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OM protein - protein search, using sw model

Run on: July 11, 2005, 09:35:34 ; Search time 39 Seconds (without alignments) 61.677 Million cell updates/sec

Perfect score: Title:

Sequence:

Scoring table: BLOSUM62DX

axaeaaekaakyaaeaaekaakaxa 25

Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB BC seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR\_79:\* pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	σ,		ω	2	1		Result
54	54	54	54	54	54.5	54.5	55	55	ទទ	55	55	56	56	56	56	56	56	57	57	57	58	58	60	63	63	63	65	71		Score
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plectin - rat	probable secreted	seed biotin-contai	ribosomal protein	amma,		DNA-directed RNA p	<u>a</u> 1	NF-180 - sea lampr	embryonic protein	ribosomal protein	o o	colicin A - Citrob	ATP-binding protei		TolA protein PA097	•		hypothetical prote	membrane spanning	membrane spanning	rifin PFB0035c - m	genome polyprotein	ATP synthase F0, B		50S ribosomal prot	$\mathbf{L}$		. hypothetical prote		Description

## ALIGNMENTS

A;Molecule type: DNA A;Residues: 1-924 <BEV> A;Residues: 1-924 <BEV> A;Cross-references: UNIPROT:Q9SU08; EMBL:AL049640; GSPDB:GN00062; ATSP:T20K18.130 A;Experimental source: cultivar Columbia; BAC clone T20K18 C;Genetics: R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew. submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15790
A;Accession: T06636 A; Map position: 4 A; Introns: 209/2; 699/3; 753/3; 785/2; 807/2; 853/3; 912/3 hypothetical protein T20K18.130 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr.1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004 A; Gene: ATSP: T20K18.130 C;Accession: Matches Query Match Match 67.6%;
Local Similarity 68.0%;
Les 17; Conservative 1 AXAEAAEKAAKYAAEAAEKAAKAXA 25 |:| | :||| |||| ||| || T06636 Mismatches Score 71; DB 2; Pred. No. 0.71; 5; Indels Length 924; 0; Gaps 0

RESULT 2

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603

AAAGARDKAAKAAAEAREKAEKAAA 627

hypothetical protein SC2E1.36 SC2E1.36 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004

C; Accession: T34804

R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1998

A; Reference number: Z21557 A; Accession: T34804

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A;Residues: 1-168 <MUR>
A;Cross-references: UNIPROT:069907;
A;Experimental source: strain A3(2) EMBL:AL023797; PIDN:CAA19411.1; GSPDB:GN00070; SCOED

Genetics: Gene: SCOEDB:SC2E1.36

Query Match Best Local S Matches 15 Similarity 61.9%; llarity 62.5%; Conservative 5 Score 65; DB 2; Pred. No. 0.81; 5; Mismatches 4. Length 168; Indels o ;: Gaps

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1 AXAEAAEKAAKYAAEAAEKAAKAX 24 |:|:||||| : || ||:|| ||:

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tolA protein - Escherichia C;Species: Escherichia coli C;Date: 07-Sep-1990 #sequen C;Accession: JV0057; B64810
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JV0057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                      A;Gene: rplS
                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:g17741210; A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; MUID:21608550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Authors: Yoo, H.; Tao, ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: circular chromosome C;Superfamily: Escherichia coli ribosomal protein
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A; Residues: 1-179 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97683
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A.; Liu, F.; Wollam, C.; Allinger, M.;
                                                                                                                                                                                                                                                                                                                             Map position: circular chromosome superfamily: Escherichia coli ribosomal protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK88423.1; PID:g15157917;
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Best Local
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    Y.; Biddle, P.; Jung, M.; Krespan,
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Pred. No. 1.4;
3; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Engineer Agrobacterium tumefaciens PMID:11743193
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Markelz, B.;
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genome polyprotein 1 - tomato ringspot virus
C;Species: tomato ringspot virus
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                                                           RESULT 7
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RiNierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin; A.S.; Gwinn, M.L.; Haft, D.H.; Kolona n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: nucleotide binding; P-loop; transmembrane protein F;14-34/Domain: transmembrane #status predicted <MSS> F;78-301/Domain: helical #status predicted <HSR> F;355-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: the authors translated the initiation codon GTG for residue R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burlar A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tolA and tolB genes and localization A;Reference number: JV0057; MUID:90078104; PMID:2687247
A;Accession: JV0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP synthase F0, B' subunit [imported] C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision C;Accession: E87294
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A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64810
                                                                                                                                                                                               C;Genetics:
A;Gene: CC0366
                                                                                                                                                                                                                                           A;Residues: 1-177 <STO>
A;Cross-references: UNIPROT:Q9AB65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960; A;Experimental source: strain K-12, substrain MG1655 C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Residues: 1-421 <BLAT>
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A; Residues: 1-42:
                                                                                                                                                                                                                                                                                           A; Molecule type:
                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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A;Experimental source: strain JM105
                                                                                                 Matches
                                                                                                                                               Query Match
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                                                AXAEAAEKAAKYAAEAAEKAAKAXA 25
ASAEAAERQAKEEAVLAEKLAAAEA
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                                                                                                                     Score 60; DB Pred. No. 3.2;
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Pred. No. 3;
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                                                                                                                                                                                                                                                PIDN:AAK22353.1; GSPDB:GN
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(strain

raspberry)

(fragment)

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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Hgasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90725
                                                                                                                                                                                                                                       membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: F90725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Gardner, M.J.; Tettelin, H.; Carucci, ; Pertea, M.; Salzberg, S.; Zhou, L.; Science 282, 1126-1132, 1998
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C;Superfamily: tomato ringspot virus genome polyprotein
C;Keywords: glycoprotein; polyprotein
F;270/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Rott, M.E.; Tremaine, J.H.; Rochon, D.M. Virology 185, 468-472, 1991
A;Title: Comparison of the 5' and 3' termini of tomato ringspot virus A;Reference number: A40787; MUID:92024112; PMID:1926788
A;Accession: A40787
                                         A; Molecule type: DNA
A; Residues: 1-394 < HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: PFB0035c
C;Superfamily: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
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C;Species: Plasmodium falciparum
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A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues:
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                                                                                    A;Status: preliminary
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;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: A71625
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1; Mismatches
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Pred. No.
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Pred. No.
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hypothetical protein T20K18.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                          A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: G85576
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                                                                 RESULT 11
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                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-394 <STO>
                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                         iller, L.; Grotbeck, E.J.; Davis,
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                           R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
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                                                                                                                                                                                  Query Match
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hypothetical protein pXO1-72 - Bacillus anthracis virulence plasmid pXO1 C;Species: Bacillus anthracis C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
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                                                              H59099
                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: cultivar
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A;Experimental source: cultivar Columbia; BAC clone T20K18
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A; Residues: 1-909 <BEV>
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                                                                                                                                                                                                                   Matches
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C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043
A; Accession:
                                                                                                                                                                                                                                            E83525
TolA protein PA0971 [imported] - Pseudomonas aeruginosa (strain PAO1)
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C;Superfamily: membrane-bound c-type cytochrome; cytochrome c
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A; Residues: 1-228 <STO>
A; Cross-references: GB:
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytochrome c, membrane-bound [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 15-Mar-2004
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A;Residues: 1-101 <OKI>
A;Cross-references: UNIPROT:Q9X342; GB:AF065404; NID:g4894216;
A;Experimental source: strain Sterne
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A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid A;Reference number: A59091; MUID:99445483; PMID:10515943
                                                                                                                                                                                                                                                                                                  RESULT 14
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                                                                                                                                                                               Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keywords: chromoprotein; heme; iron; metalloprotein;81,84/Binding site: heme (Cys) (covalent) #status predicted;81,84/Binding site: heme iron (His) (axial ligand) #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Superfamily: Bacillus anthracis virulence plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;150/Binding site:
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Pred. No.
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K.; Lim,
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                                                                                                                                                                    A;Cross-references: UNIPROT:Q8YPL1; GB:BA000019; PIDN:BAB75882.1; PID:g17133318; GSPDB:GN
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-564 <KUR>
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Query Match Best Local S

Matches

l Similarity

Conservative

5

53.3%; 61.9%;

Score 56; Pred. No.

DB 25;

2

Length 564 Indels

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Pred. No. 25; 5; Mismatches

;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding

protein of ABC transporter all4183 [imported] -

Nostoc sp.

(strain PCC

strain PCC 09-Jul-2004

7120

Watanabe, ; Yasuda, N

**™** 

Iriguchi

Cyanobacterium

Anal လ

all4183

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <STO>
A;Cross-references: UNIPROT:P50600;
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                           R;Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera patho A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82152
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                                                                                                                                            A; Map position:
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A;Experimental source: serogroup Ol; strain N16961; biotype El Tor.
                                                                                                                                                                                                                                           A; Residues: 1-356 <HEI>
                                                                                                                                                                                                                                                          A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                   ;Gene: VC1837
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AKAEQERLAKEKAAKEAADKAKKEKERAAKAEA
                                  AXAE----AAEKAAKYAAEAA----EKAAKAXA
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Pred. No.
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                                                                                                          Length 356;
                                                                                                                                                                                                                                                                                                                                    pathogen Vibrio cholerae
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A;Cross-references: GB:X01008; GB:X00034; NID:g40459; PIDN:CAA25503.1; R;Morion, J.; Lloubes, R.; Chartier, M.; Bonicel, J.; Lazdunski, C. EMBO J. 2, 787-789, 1983
A;Title: Nucleotide sequence of promoter, operator and amino-terminal rA;Reference number: 140777; MUID:84057757; PMID:6641715
A;Accession: 140777
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C;Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: I40784; A03504; T40777
C;Accession: J; Chartier, M; Bidaud, M; Lazdunski, C.
Mol. Gen. Genet. 21, 231-243, 1988
A;Title: The complete nucleotide sequence of the colicinogenic plasmid ColA. High extent A;Reference number: I40778; MUID:88174422; PMID:2832701
                                                                                                                                                      R;Scott, G.K.; Davies, P.L.; Shears, M.A.; Fletcher, G.L. Eur. J. Blochem. 168, 629-633, 1987
A;Title: Structural variations in the alanine-rich antifreeze A;Reference number: S02376; MUID:88029483; PMID:3665937
A;Accession: S02376
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S02376
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                        A;Cross-references: UNIPROT:P09031; EMBL:X06356; NID:g64041; PIDN:CAA29655.1; PID:g64042A;Note: part of this sequence, including the amino end of the mature protein, was confix C;Superfamily: antifreeze protein
                                                                                                                                                                                                                                                                                                       antifreeze protein precursor - yellowtail flounder
C;Species: Limanda ferruginea (yellowtail flounder)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
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A;Experimental source: plasmid ColA
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A;Residues: 1-53,'X',55-70 <RE2>
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A; Residues: 1-592 < MOR>
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                                                                                                      A; Molecule type: mRNA
A; Residues: 1-97 < SCO>
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;Keywords: antibiotic; bacteriocin; toxin; transmembrane protein
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I51116
NF-180 - sea lamprey
C;Species: Petromyzo
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RESULT 20
S04909
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A;Reference number: Z21718
A;Accession: T37490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S04909

R;Franz, G; Hatzopoulos, P.; Jones, T.J.; Krauss, M.; Sung, P.; Jones, T.J.; Krauss, M.; Sung, P.; Jones, T.J.; Krauss, M.; Sung, P.; Jones, Genet. 218, 143-151, 1989

A;Title: Molecular and genetic analysis of an embryonic gene, A;Reference number: S04909; MUID:89384429; PMID:2571069

A;Accession: S04909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1-23/Domain: signal sequence #status predicted <SIG>F;24-48/Domain: propeptide #status predicted <PRO>F;49-96/Product: antifreeze protein #status predicted
                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P20075; GB:X16131; NID:g18333; PIDN:CAA34258.2; PID:g4902464 C;Superfamily: pea seed biotin-containing protein
                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-555 < FRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Daucus carota (carrot)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  embryonic protein DC8 (clone 8/10) - carrot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 103/3
C;Superfamily: rat acidic ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 1
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A;Experimental source: strain 972h-; cosmid c1071
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15; Conserv
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Similarity 56.0%;
14; Conservative
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Pred. No. 7.1;
                                                                                                                                  Pred. No. 32;
5; Mismatches
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Pred. No. 7.9;
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Petromyzon

marinus (sea lamprey)

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R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Do A;Title: Complete Genome Sequence of a virulent isolate of Strep
                                                                                            A; Status F--- DNA
A; Molecule type: DNA
A; Residues: 1-1203 < KUR>
A; Cross-references: UNIPROT: Q97NQ7;
A; Cross-references: Etrain TIGR4
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                                                                                                                                                                                                                                                                                                                                                  C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95229
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A;Residues: 1-1147 <SEE>
A;Cross-references: UNIPROT:087848;
A;Experimental source: strain A3(2)
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A; Reference number: Z21570
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A; Residues: 1-1110 < JAC>
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                                                                                                                                                                                             A;Reference number: A95000; MUID:21357209; A;Accession: C95229
                                                                                                                                                                                                                                                                                                                                                                                                             DNA-directed RNA polymerase, beta chain [imported]
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C;Superfamily: neurofilament triplet H protein
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                                        DNA-directed RNA polymerase beta chain
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Brain Res. 29, 43-52, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.4%;
    .98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB Pred. No. 59; 7; Mismatches
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Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            744
                                                                                                                GB:AE005672; PIDN:AAK76028.1; PID:g14973467;
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  54.5;
                                                                                                                                                                                                                 PMID:11463916
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  BB
                                                                                                                                                                                                                                   Venter, J.C.; Dougherty, isolate of Streptococcus
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2:

    Streptococcus pneumoniae

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Length 1203;
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Radune, D.; Holtzapple,
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                                                                                                                                                                                                                                 pneumoniae.
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C;Superf
ribosomal protein S2 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 C;Accession: T34809
                                                                          RESULT
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A26721
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-217 < kNO>
A;Residues: 1-217 < kNO>
A;Cross-references: UNIPROT:P07796; GB:M16033; NID:g161517; PIDN:AAA30059.1;
A;Cross-references: UNIPROT:P07796; GB:M16033; NID:g161517; PIDN:AAA30059.1;
C;Superfamily: histone H1
C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
F;2-217/Product: histone H1-gamma, embryonic #status predicted <MAT>
                                                                                                                                                                                                                                                                                                               R;Knowles, J.A.; Lai, Z.C.; Childs, G.J. Mol. Cell. Biol. 7, 478-485, 1987
A;Title: Isolation, characterization, and 6
A;Reference number: A26721; MUID:87172742;
A;Accession: A26721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, & e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, y, P.; Sun, P.M.; Winkler, M.E. J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                       histone H1-gamma, embryonic - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1216 <KUR>
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                                                                                        13;
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                                                                                                           Score 54;
Pred. No.
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Pred. No. 70;
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212
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#text\_change

09-Jul-2004

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C;Accession: T07064
R;Hsing, Y.C.; Tsou, C.H.; Hsu, T.F.; Chen, Z.Y.; Hsieh, K.L
Plant Mol. Biol. 38, 481-490, 1998
A;Title: Tissue- and stage-specific expression of a soybean
A;Reference number: Z15895; MUID:98418627; PMID:9747855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:039846; EMBB:U59626; NID:g1389896; PIDN:AAC61783.1; A;Experimental source: strain Shi-Shi; cotyledon C;Superfamily: pea seed blockin-containing protein C;Keywords: blockin binding; seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seed biotin-containing protein LEA [validated] - soybean
C;Species: Glycine max (soybean)
C;Date: 01-Sep-2000 #sequence_revision 01-Sep-2000 #text
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A;Cross-references: UNIPROT:031212;
A;Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                     C;Accession: T34852
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.;
submitted to the EMBL Data Library, February 1999
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A; Residues: 1-643 < HSI>
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                                                                                                                                                                                                                                                                  A;Reference number: Z21559
A;Accession: T34852
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Best Local S
Matches 14
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;Residues: 1-1156 <OLI>
                                                                                                                                                                    Cross-references: UNIPROT:Q9Z5A4; EMBL:AL035478; PIDN:CAB36606.1; GSPDB:GN00070; Experimental source: strain A3(2)
                                                                                                                                                                                                                                           ;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                          Species: Streptomyces coelicolor;Date: 05-Nov-1999 #text_change 09-Jul-2004;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
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family: Escherichia coli ribosomal
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58.3%;
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; Pred. No. 47;
3; Mismatches
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Pred. No.
                                                                   Score 54; DB
Pred. No. 77;
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                                                                                        Length 1156;
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R;Kenleuwern, 1894, 1994
Nature 372, 804-809, 1994
A;Title: XL-alpha-s is a new type of G protein.
A;Title: XL-alpha-s is a new type of G protein.
Page 1997272
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S52418
GTP-binding regulatory protein Gs alpha-XL chain N;Alternate names: G protein XL-alpha-s C;Species: Rattus norvegicus (Norway rat) C;Date: 14-Jul-1995 #sequence_revision 10-Nov-199 C;Accession: S52418
C;Accession: S52418
C;Accession: Matthey, J.; Huttner, W.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
A39638
                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: antifreeze; blocked amino end; plasma F;9-45/Region: alanine-rich F;1/Modified site: blocked amino end (Met) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Structures of shorthorn sculpin antifreeze polypeptides A;Reference number: A91150; MUID:85285003; PMID:4029130 A;Accession: A05163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plectin - rat
C;Species: Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antifreeze protein SS-8 - shorthorn sculpin
C;Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: cytoskeleton; transmembrane protein F;6-103/Domain: ribosomal protein S10 homology F;184-399/Domain: alpha-actinin actin-binding d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Cloning and sequencing of rat plectin indicates a 466-kD polypeptide chain with A;Reference number: A39638; MUID:91268156; PMID:2050743 A;Accession: A39638
                                                                                                                                                                      RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P04368 C;Superfamily: antifreeze protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 1-45 < HEW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hew, C.L.; Joshi, S.; Wang, N.C.;
Eur. J. Biochem. 151, 167-172, 1985
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C;Superfamily: plectin; alpha-actinin actin-binding domain homology; ribosomal protein S
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A; Residues: 1-4687 < WIC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Rattus norvegicus (Norway rat)
Date: 10-Sep-1999 #sequence_revision 10;
Accession: A39638; S21876
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Pred. No. 2.6e+02;
7; Mismatches 6
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10-Nov-1995

#text\_change

02-Feb-2001

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A;Contents: annotation; assignment of start codon
A;Note: experimental data from this paper suggest that the translation is initiated at p
C;Keywords: GTP binding; nucleotide binding; P-loop; signal transduction
F;132-846/Product: GTP-binding regulatory protein Gs alpha-XL chain #status experimental
F;499-506/Region: nucleotide-binding motif A (P-loop)
F;744-747/Region: GTP-binding NKXD motif
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                                                                                                                                                                                                                                            Figure Mol. Biol. 18, 143-146, 1992
A;Title: Two GC-rich DNA elements of Chlamydomonas reinhardtii with A;Reference number: S19113; MUID:92119224; PMID:1731966
A;Accession: S19114
                                                                                                                                                                                                                                                                                                                                                                     cgcr-1 protein - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Date: 13-Jan-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P20617
C;Superfamily: antifreeze protein
C;Keywords: antifreeze; blocked amino end
F;1/Modified site: blocked amino end (Met)
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FDF18G
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                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                              C;Accession: S19114
R;Wakarchuk, W.W.; Mueller, F.W.; Beck, C.F.
Plant Mol. Biol. 18, 143-146, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antifreeze protein GS-8 - grubby sculpin
C;Species: Myoxocephalus aenaeus (grubby sculpin)
C;Date: 31-Dec_1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
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A; Residues: 1-846 < KEH>
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A;Residues: 1-40 <CHA>
                                                                                                                                        ;Residues: 1-205 <WAK>;Cross-references: UNIPROT:Q39597; EMBL:X17207;Superfamily: phage lambda hypothetical protein 401
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                 AXAEAAEKAAKYAAEAAEKAAKAXA
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                                                         Conservative
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                                                       6
                                                       Score 53; DB
Pred. No. 23;
6; Mismatches
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3; Mismatches
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RyPearson, D.; Churcher, ......
Rypearson, D.; Churcher, .....
submitted to the EMBL Data Library,
submitted to the EMBL Data Library,
submitted to the EMBL Data Library,
                                                                        C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision
C;Accession: T38147
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 AAAQAAAQAAAERAAAAQAAAQAAA 148
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A;Cross-references: GB:AL513382; PIDN:CAD05209.1; C;Genetics: A;Gene: STY0793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG0592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tolA protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0592 C;Accession: AG0592 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churc th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far
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                                                                                                                                                                           A;Gene: tolA
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                                                                                                                                                                                                                 A; Cross-references: UNIPROT: Q8ZGZ2;
                                                                                                                                                                                                                                       A;Residues:
                                                                                                                                                                                                                                                         A; Molecule type:
                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                    A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AC0138
                                                                                                                                                                                                                                                                                                                                                                      Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TolA colicin import membrane protein [imported] - Yersinia pestis (strain
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A;Residues: 1-376 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Yersinia pestis
Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                                                          Query Match
Best Local Similarity
Matches 13; Conserv
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Best Local
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212 KAVEVAEKAAADAAEKKAAADA 23:
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                                        ЕААЕКААКҮААЕААЕКААКАХА 25
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Pred. No. 38;
6; Mismatches
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                                                                                     3; Mismatches
                                                                                                     Score 53; DB
Pred. No. 39;
                                                                                                                                                                                                                 GB:AL590842; PIDN:CAC89966.1;
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                                                                                                                           Length 388
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, L.; White, N.; Farrar,
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                                                                                                                                                                                                                 PID:g15979190;
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dolichyl-phosphate-mannose-protein mannosyl transferase

Churcher, C.M.; Barrell, B.G.;

September 1997

03-Dec-1999 #text\_change 09-Jul-2004 Rajandream, M.A.; Wood, V.

fission yeast (Schizosaccharom)

RESULT 36

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repetitive protein antigen 69/70 - Trypanosoma cruzi (fragment)
C;Species: Trypanosoma cruzi
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: H83437
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PA1669 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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C;Superfamily: dolichyl-phosphate-mannose-protein mannosyltransferase
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A;Cross-references: UNIPROT:013898; EMBL:Z99295; PIDN:CAB16577.1; GSPDB:GN00066;
A;Experimental source: strain 972h-; cosmid c22A12
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                                                                                              A;Cross-references: UNIPROT:Q7M3W1
C;Superfamily: varicella-zoster virus
C;Keywords: tandem repeat
                                                                                                                                                         A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-97 <HOF>
                                                                                                                                                                                                               A;Title: Trypanosoma cruzi expresses diverse repetitive protein antigens
A;Reference number: A60110; MUID:89277508; PMID:2659529
A;Accession: G60110
                                                                                                                                                                                                                                                                       R;Hoft, D.F.; Kim, K.S.; Otsu, K.; Infect. Immun. 57, 1959-1967, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9I356; GB:AE004594; GB:AE004091; NID:g9947630; PIDN:AAG0505
A;Experimental source: strain PAO1
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Matches
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    Local Similarity 56.
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                    49.5%;
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  Score 52; DB Pred. No. 16; 3; Mismatches
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Pred. No. 1.2e+02;
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Pred. No. 80;
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K.; Lim,
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C;Species: Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision ?^ -
C;Accession: A25550
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Althors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                               A;Gene:
C;Superf
                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: clone C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26386
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A;Accession: T26386
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A;Residues: 1-147 <STO>
A;Cross-references: UNIPROT:Q9C674; GB:AE005172; NID:g11079518; PIDN:AAG29229.1; GSPDB:G
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A;Accession: D86389
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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family: human S-phase kinase-associated protein
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                                      #sequence_revision 30-Jun-1988
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52.6%;
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Pred. No.
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                                   #text_change 09-Jul-2004
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Marziali,
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ABA-inducible protein, landform-specific - Riccia fluitans C;Species: Riccia fluitans C;Species: Riccia fluitans C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_cb C;Accession: S58219
R;Hellwege, E.M.; Dietz, K.J.; Hartung, W. submitted to the EMBL Data Library, July 1995
A;Bescription: Abscisic acid causes changes in gene express A;Reference number: S58219
A;Accession: S58219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Parechinus angulosus (angulate urchin)
C;Date: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 09-Jul-2004
C;Accession: A91090; A91091; A02586
R;Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, B. Bur. J. Biochem. 104, 559-566, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus arminal cyanogen bromide peptides.
A;Reference number: A91090; MUID:80158831; PMID:6767609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P02256

R;Strickland, W.N.; Strickland, M.; Brandt, W.F.;

Eur. J. Biochem. 104, 567-578, 1980

A;Title: The primary structure of histone H1 from

A;Reference number: A91091; MUID:80156832; PMID:73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-210 < KNO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-8133, 1986
A;Title: Comparison of the late H1 histone
A;Reference number: A25550; MUID:87040778;
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C;Keywords:
                                                     A;Cross-references: UNIPROT:Q41154; EMBL:X89041; NID:g929818; PIDN:CAA61439.1; PID:g9298
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C;Superfamily: histone H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A91091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-248 <STR>
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Best Local S
Matches 13
                                                                         ;Molecule type: mRNA
;Residues: 1-288 <HEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Keywords:
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 Query Match
Best Local Similarity
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Parechinus angulosus (angulate urchin)
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13; Conserv
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DB
40;
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secs

completed: July 11,

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RESULT
S41061
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C;Superfamily: transcription antitermination factor nusG
C;Keywords: transcription antitermination; transcription
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S32234
                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Streptomyces griseus
A;Variety: strain IFO13350
C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                   probable transcription antitermination C;Species: Streptomyces ~~---
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                                                                                                                             A;Description: may be involved in antibiotics production C;Superfamily: transcription antitermination factor nusG
                                                                                                                                                                                                                                                                                                               R;Miyake, K.; Onaka, H.; Horinouchi, S.; Beppu, T. Biochim. Biophys. Acta 1217, 97-100, 1994
A;Ticle: Organization and nucleotide sequence of the secE-nusGA;Reference number: S41059; MUID:94114580; PMID:8286423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: nusG
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                                                                                                                                                                                 A;Start codon: GTG
                                                                                                                                                                                                 A;Gene:
                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P36260; EMBL:D17464; NID:g436786; PIDN:BAA04281.1; PID:g4838
A;Experimental source: strain IFO13350
                                                                                                                                                                                                                                                                  A;Residues: 1-294 <MIY>
                                                                                                                                                                                                                                                                              A; Molecule type:
                                                                                                                                                                                                                                                                                                A; Accession: S41061
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A;Cross-references: UNIPROT:P36260;
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;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
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                                                                                 Score 52;
Pred. No.
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                                                                 Indels
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grj

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: July 11, 2005, 09:24:04 ; Search time 167 Seconds (without alignments) 76.659 Million cell updates/sec

Sequence: Title: Perfect score: SEQ1 1 axaeaaekaakyaaeaaekaakaxa 25

BLOSUM62DX Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Regult No.		Query Match	Length	BB	ID	Description
1	71	67.6	485	N	Q8RXD0	Q8rxd0 arabidopsis
22	71	67.6	924	Ŋ	Q9SU08	arabidops
ω	67	'n	278	N	Q7Q0M9	anopheles
4	65	61.9	168	N	069907	streptomyc
<sub>U</sub>	63	0	179	ب	RL19_AGRT5	
თ	63	0	413	ĸ	Q83SĀ1	Q83sal shigella fl
7	63	60.0	421	بر	TOLA_ECOLI	P19934 escherichia
œ	63	60.0	421	N	Q8FJT1	Q8fjt1 escherichia
9	61	58.1	441	N	Q6N8X8	Q6n8x8 rhodopseudo
10	61	58.1	593	N	Q8ZNE5	
11		.7	711	N	Q7Z3F5	Q7z3f5 homo sapien
12		7.	730	μ	ELS_HUMAN	
13	O	57.6	757	N	Q14234	4 homo
14	60.5	57.6	757	N	Q75MU5	5 homo
15	60	57.1	105	N	Q6N503	rhode
16	60	57.1	177	N	Q9AB65	_
17	60	57.1	371	N	Q6N4V4	Q6n4v4 rhodopseudo
18	60	57.1	572	N	Q6NH65	Q6nh65 corynebacte
19	60	7.	738	N	Q6UBQ3	Q6ubq3 chlamydomon
20	σ	57.1	899	N	Q8NIZ0	
21	٠	ο.	531	N	Q7PNQ9	Q7pnq9 anopheles g
22	9		647	ผ	Q891E4	
23	59	٥.	347	N	Q9RKL9	_
24	59	56.2	389	N	Q9CM70	_
25	59		1020	Ν	Q86PC3	ω
26	59		1020	N	Q9W2J2	
27	59	6	1069	N	Q86BG1	-
28	8	Š	181	N	Q64SR3	
29	θ.	<u>ن</u>	496	N	Q8VQW6	
30	٠	'n	508	N	Q9VGD2	
31	58.5	55.7	664	N	Q9VGD3	

58.5 55.7 1171 2 QBSWEY 58.5 55.7 1171 2 QPSWEY 58.5 55.7 1171 2 QPSWEZ 58.5 55.7 1171 2 QPSWEZ 58.5 55.2 92 2 QPDF23 58.5 55.2 124 2 QTV6K8 58.5 52.2 187 2 QFWB7 58.5 52.2 558 2 QTRWB7 58.5 52.2 575 2 QFFF71 58.5 55.2 860 2 QBSWM9 58.5 52.2 197 1 POLI_TORVR 57.5 54.8 638 2 QBSJE3 57.5 54.3 190 2 QBSJE3 57.5 54.3 394 2 QBSJE3 57.5 54.3 394 2 QBSJE3 57.5 54.3 394 2 QBSJE3	55.7 11171 55.7 1172 55.2 92 2 55.2 387 2 55.2 558 2 55.2 575 2 55.2 660 2 55.2 809 2 55.2 2197 1 54.8 638 2 54.3 394 2 54.3 394 2	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	3.2
1171 124 2 387 558 575 600 2 2197 1 190 2 508 2 508 2	1171 2 Q9P3E2 Q9P3e2 12 Q9P3E2 Q9P3e2 2 Q9DF23 Q9df23 124 2 Q7V6KB 387 2 Q96H13 Q7V6KB 387 2 Q7RWB7 575 2 Q6PF71 Q6pf71 660 2 Q88YM9 P90534 2197 1 POLI_TRVR P29150 638 2 Q89IE3 190 2 Q89SE3 Q89SE3 190 2 Q89SE3 190 2 Q875A8 Q875A8	57	57	57	57.5	58	58	58	58	58	58	58	58	58.5	50.5
, , , , , , , , , , , , , , , , , , ,	2 QSSM1/ 2 QSP3E2 2 QSP3E2 2 QSDF23 2 QVKKB 2 QS6113 2 QYKKB 2 QS6113 2 QYRWB7 2 QSF71 2 QSF71 2 QSF771 2 QSF751 2 QSF751	54.3	54.3	54.3	54.8	55.2	55.2	55.2	55.2	55.2	55.2	55.2	55.2	55.7	55./
2 Q9P3E2 2 Q9P3E2 2 Q9DF23 2 Q9DF23 2 Q9G1B3 2 Q9F8B1 2 Q6PF71 2 Q6PF71 2 Q6PF71 2 Q6SYM9 2 P9053M9 2 P90515 2 Q891E3 2 Q891E3 2 Q89565 2 Q875A8	Qoggae, Qoggae, Qoff23 Qoff23 Qoff23 Qoff23 Qoff71 Qoff71 Qoff71 Qoff71 Qoff9150 Qof	508	394	190	638	2197	809	660	575	558	387	124	92	1171	694
QSSW17 QSP3E2 QSP5E3 Q7V6K8 QS6E13 Q7RWB7 Q6EP71 Q6EP71 Q6EP71 Q6EP71 Q8EYM9 P90534 P011, TORVR Q891E3 Q891E3 Q89265 Q875A8	Qeswc, Qegaez, Qedf23 Qedf23 Qef123 Qef123 Qef123 Qef121 Qeff71 Qeff71 Qeff71 Qeff71 Qeff860 Qeff860 Qeff860 Qeff860 Qeff860	N	N	N	N	۲	N	N	N	N	N	N	N	N	٨
		Q875A8	Q8X965	015860	Q89IE3	POL1_TORVR	P90534	Q88YM9	Q6PF71	Q7RWB7	096113	Q7V6K8	Q9DF23	Q9P3E2	Cacata

## ALIGNMENTS

RESULT Q9SUOB ID Q AC Q DT O	Quer Best Matc	RA R	82	RESULT QBRXDO ID Q AC Q DT 0 DT 0 DT 0 DT 0 DT 0
IT 2 98 Q9SUO8 PRELIMINARY; PRT; 924 AA. Q9SUO8; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	Query March 67.6%; Score 71; DB 2; Length 485; Best Local Similarity 68.0%; Pred. No. 2.1; Matches 17; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  1 AXABAAEKAAKYAABAAEKAAKAXA 25  1	ECKET J., Theologis A., Davis R.W.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.  [2] [2] [3] SEQUENCE FROM N.A. SHIND P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P., Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P., Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  EMBL; AY081334; AAL91233.1; EMBL; BT009679; AAP81797.1; HSSP; Q27974; INZ6. InterPro; IRR011633; DnaJ_N. SMART; SM00271; DnaJ; 1. SMART; SM00271; DnaJ; 1.	liana (Mouse-eddiplantae; Stramagnoliophyta; Magnoliophyta; assicales; Brat; .A	JT 1  OBRXDO PRELIMINARY; PRT; 485 AA.  OBRXDO;  O1-JUN-2002 (TrEMBLrel. 21, Created)  O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)  O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)  Auxilin-like protein (At4g12780).

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RESULT
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Best Local
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Anopheles Genome Sequencing Consortium;
Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ribosomal protein L13P family.
-!- CAUTION: The sequence shown here is derived from an
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7Q0M9;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence up
01-MAR-2004 (TrEMBLrel. 26, Last annotation
01-MAR-2004 (TrEMBLrel. 28, Last annotation
AgCP8317 (Fragment).
Name=agCG54338; ORFNames=ENSANGG000000011932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bevan M.,
Bancroft I
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids;
eurosids_II_Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                    EMBL; AAAB01008980; EAA14246.1; HSSP; O59300; 1J3A.
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Name=T20K18.130; Syno
GO; GO:0015934; C:large ribosomal subunit; 1
GO; GO:0003735; F:structural constituent of
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR005822; Ribosomal L13.
InterPro; IPR005755; Ribosomal L13e/a.
Pfam; PF00572; Ribosomal_L13; T.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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bmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
BL; AL049640; CAB40995.1; -.
BL; AL161534; CAB78320.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis sequencing project; mitted (APR-1999) to the EMBL/GenBank/DDBJ databases
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; 027974; 1NZ6.
erPro; IPR001623; DnaJ_N.
erT; SM00271; DnaJ; 1.
er2 AA; 102223 MW; 2
                                                                                                                                                                                                   preliminary data.
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I., Mewes H.W.,
1 (APR-1999) to t
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68.0%;
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Pred. No. 3.5;
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STRAIN=A3(2) / M145;

MEDLINE=2196410; PubMed=12000953; DOI=10.1038/417141a;

MEDLINE=2196410; PubMed=12000953; DOI=10.1038/417141a;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Thumson C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Marren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                         Q8UBZ5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
25-OCT-2004 (Rel. 45, Last annotation
50S ribosomal protein L19.
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AGRT5
RL19_1
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TIGRFAMS; TIGRO1077; L13 A E; 1.
PROSITE; PS00783; RIBOSOMAL L13; 1.
Ribonucleoprotein; Ribosomal protein.
NON TER 1 1
SEQUENCE 278 AA; 31601 MW; D47C71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939124; CAA19411.1;
                                         Name=rplS; OrderedLocusNames=Atu2703, AGR C 4900;
Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
Bacteria; Proteobacteria; Rhizaproteobacteria; Rhiza
Batizobiaceae; Rhizobium/Agrobacterium group; Agrobac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; Hypothetical protein. SEQUENCE 168 AA; 17934 MW; 72063B195040BD6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.
Bacteria; Actinobacteria;
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01-JUN-2003
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             NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1902;
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(TTEMBLrel. 07, Last sequence update)
(TTEMBLrel. 24, Last annotation update)
1 protein SCO5619.
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Streptomycetaceae; Streptomyces.
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62.5%;
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                                           group; Agrobacterium.
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Matches 18
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           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Membrane spanning protein, required for outer membrane integrity.
Name=tclA; OrderedLocusNames=S0571, SF0558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.", Science 294.2323.2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01245; Ribosomal L19; I. PRINTS; PR00061; RIBOSOMALL19. ProDom; PD002979; Ribosomal L19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE009216; AAL43684.1;
EMBL; AE008183; AAK88423.1;
PIR; AF2908; AF2908.
PIR; F97683; F97683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Poundel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Wollam C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cilled C., Cowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                         Q83SA1; Q7C2Q4;
01-JUN-2003 (TrEMBLrel.
                                                                                                                                  Q83SA1
                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR01024; rpls_bact; 1. PROSITE; PS01015; RIBOSOMAL L19; 1. Complete proteome; Ribosomal protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_00402; -; 1.
InterPro; IPR001857; Ribosomal_L19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interface and may play a role in the structure and function aminoacyl-tRNA binding site (By similarity).
SIMILARITY: Belongs to the ribosomal protein L19P family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: This protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-trna binding site (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                              proteome;
179 AA;
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                                                                                                                                                                                                                                                                                                                                                                                19474 MW;
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                                                                                                                                                                                                                                                                                                                      Score 63;
Pred. No.
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7.8;
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nax/gkf566;
Jin Q., Yuan Z., Xu J., Mang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seg
25-JAN-2005 (Rel. 46, Last ann
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DOI=10.1128/IAI.71.5.2775-2786.2003;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., De Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                            Escherichia coli.";
J. Bacteriol. 171:6600-6609(1989)
                                                                                                                                                                                                                                                                                                   MEDLINE=700702000 NEW MEDITION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=tolA; Synonyms=cim, excC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12 / JM105;
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Pred. No. 15;
6; Mismatches
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J., Darling /
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use by non-profit institute of Bioinformatics and the EMBL outst use by non-profit institutions as long as its content is in entities requires a license agreement.
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"A 718-kb
                                                                        TRANSMEM
DOMAIN
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                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                          EMBL; M28232; AAA24683.1; -.
EMBL; U00096; AAC73833.1; -.
EMBL; D90713; BAA55405.1; -.
PIR; JV0057; JV0057.
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MEDLINE=99332679; PubMed=10404600; DOI=10.1016/S0969-2126(99)80092-6;
Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A.;
"Filamentous phage infection: crystal structure of g3p in complex with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91296736; PubMed=2068069;
Levengood S.K., Beyer W.F. Jr., Webster R.E.;
"Tolh: a membrane protein involved in colicin uptake
extended helical region.";
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EchoBASE; F
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EMBO J. 15:6408-6415(1996).
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                                                                                                                                      3D-structure;
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                                                                                                                     inner membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Involved in the tonB-independent uptake of group A colicins (colicins A, El, E2, E3, and K). Necessary for the colicins to reach their respective targets after initial binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the bacteria. Also involved bacteriophage DNA.
                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome sequence of Escherichia coli K-12.", nce 277:1453-1474 (1997).
                                                                                                                                                                                                                                                                                    s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                 EG11007; tolA.
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6519; TolA; 1.
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EB1000; -.
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                                                                                                                                  Bacteriocin transport; Complete proteome;
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13 Cytoplasmic (Potential)
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                         Domain II (alpha-helical).

Domain III (functional).

13 X tandem repeats of [EDA]-K(1,2)-
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SEQUENCE
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MEDLLINE=22388234; PubMed=112471157; DOI=10.1073/pnas.252529799;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Str

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome se
of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
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01-MAR-2004 (TrEMBLrel.
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Pfam; PF06519; TolA;
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Enterobacteriaceae; Escherichia.
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Pred. No. 16;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence to 05-JUL-2004 (TrEMBLrel. 27, Last annotation Compa/MotB domain, possible porin precursor. OrderedLocusNames=RPA1774; Rhodopseudomonas ~~1
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Q8ZNE5;
01-MAR-2002
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative von Willebrand factor, VWF type A domain.
Name=yfbK; OrdereduocusNames=STM2315;
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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"Complete genome sequence of the metabolically versatile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIN'S; PRO1021; OMPADOMAIN.

ProDom; PD000930; OmpA/MotB; 1.

Complete proteome; Porin; Signal.

SIGNAL 27 Potential.
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Nat. Biotechnol. 22:55-61(2004).
-!-SIMILARITY: Belongs to the ompA family.
EMBL; BX572598; CAE27215.1;
-GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0009279; C:outer membrane (sensu Gram-negative)
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STRAIN=CGA009 / ATCC BAA-98;
PubMed=14704707; DOI=10.1038/nbt923;
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                                                  McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae;
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InterPro; IPR006664; Bac_OmpA.
InterPro; IPR006665; OmpA/MotB.
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NCBI_TaxID=1076;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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                             Waterston R., Wilson R.K.;
                                                                                                                                                                          MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
'Complete genome
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sequence of Salmonella enterica serovar Typhimurium
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62.5%;
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Pred. No.
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EMBL; AB008803; AAL21216.1; -
Pfam; PF00092; VWA; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                  HUMAN STANDARD; PRT; 730 AA.

P15502; Q14233; Q14238;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Elastin precursor (Tropoelastin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TIEMBLrel. 25, Created)
01-MAR-2004 (TIEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686F06102.
Name-DKFZp686F06102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Human fetal kidney;
Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wie
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX537939; CAD97910.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 593 AA;
Indik Z., Yeh H., Ornstein-Goldstein N., Sheppard P., Rosenbloom J.C., Peltonen L., Rosenbloom J.; Peltonen C., Peltonen Lastin mRNA indicated analysis of cloned genomic and complementary DNA,"; Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987).
                                                                                                                 Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 711 AA; 6
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Mammalia; Eutheria; Primates;
                                                            SEQUENCE FROM N.A. (ISOFORM B).
MEDLINE=87289668; PubMed=3039501;
                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001451; Hexapep_transf.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN
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                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                         Name=ELN
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Pred. No.
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Pred. No. 4:
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J. Invest. Dermatol. 91:458-464(1988).
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MEDLINE=96291399; PubMed=8689688; DOI=10.1016/S0092-8674(00)80077-X;
Frangiskakis J.M., Ewart A.K., Morris C.A., Mervis C.B., Bertrand J.
Robinson B.F., Klein B.P., Ensing G.J., Everett L.A., Green E.D.,
Proeschel C., Gutowski N.J., Noble M., Atkinson D.L., Odelberg S.J.,
Vesting M.C.,
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SEQUENCE FROM N.A. (ISOFORM TISSUE=Skin fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fazio M.J., Olsen D.R., Kuivaniemi H., Chu M.L., Davidson J.M., Rosenbloom J., Uitto J., "Isolation and characterization of human elastin cDNAs, and age
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99091639; PubMed=9873040; DOI=10.1074/jbc.274.2.981; Zhang M.-C., He L., Giro M., Yong S.L., Tiller G.E., Davidson "Cutis laxa arising from frameshift mutations in exon 30 of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elastin gene (ELN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Major structural protein of tissues such as aorta and nuchal ligament, which must expand rapidly and recover complete. SUBUNIT: The polymeric elastin chains are cross-linked together into an extensible 3D network.
                                            diverticula, pulmonary artery stenosis and pyloric stenosis. DISEASE: Haploinsufficiency of ELN may be the cause of certain cardiovascular and musculo-skeletal abnormalities observed in Williams-Beuren syndrome (WBS) [MIM:194050]. WBS is a rare developmental disorder and a contiguous gene deletion syndrome involving genes from chromosome band 7q11.23.

DISEASE: Defects in ELN are the cause of supravalvular aortic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P15502-2; Sequence=VSP_004243;
PTM: The crosslinks are made of deaminated Lys.
DISEASE: Defects in ELN are a cause of autosomal dominant cultaxa [MIM:123700]. Cutis laxa is a rare connective tissue dicharacterized by loose, hyperextensible skin with decreased controlled to the controlled by loose.
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                                                                                                                                                                                                                                                                                                                                                                                                                       resilience and elasticity leading to a premature aged appearance The skin changes are often accompanied by extracutaneous manifestations, including pulmonary emphysema, bladder
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86:59-69(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comment=Additional isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence=Displayed;
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expression in cultured skin
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narrowing
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RESULT Q14234 ID Q1 AC Q1 DT 01 DT 01

Q14234 Q14234; 01-NOV-1996 01-NOV-1996

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Best Local S
Matches 17
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EMBL; X15603; C....
& PIR; A32707; EAHU.
R HSSP; P50099; 1ZFJ.
Genew; HGNC:3327; ELN.
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This SWISS-PROT entry is copyright. It is properties and the swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics are no restrictions to the European Bioinformatics Institute. There are no restrictions the European Bioinformatics Institutions as long as its content is in no way have non-profit institutions as long as its content and for commercial and commerci
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MIM; 130160; -.
MIM; 123700; -.
MIM; 194050; -.
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GO; GO:0005578; C:extracellular matrix; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0008875; P:circulation; TAS.
GO; GO:0009887; P:organogenesis; TAS.
GO; GO:0009887; P:respiratory gaseous exchange; TAS.
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VARSPLIC
                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M36860; AAA52382.1;
M24782; AAA53190.1;
U62292; AAB17544.1;
X15603; CAA33627.1;
441
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M17276;
M17277;
M17277;
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M17265;
                                                                         l Similarity
                                                                                                                                                                                                                                                                                                  PR01500;
                                АХАЕАЛЕКААКҮ----АЛЕАЛЕКААКАХ 24
AQAAAAAKAAKYGVGTPAAAAAKAAAKAA 469
                                                                                                                                                                                                                                                                                                                    IPR003979;
                                                                                                                                               730 AA;
                                                                                                                                                                                                                                                                               splicing; Repeat;
                                                                         Conservative
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477
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58.6%;
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                                                                                                                                             Blastin.
By similarity.
By similarity.
Missing (in isoform 2
/FTId=VSP 004243.
W; AB06D15BA567AE46 CR
                                                                     Score 60.5; D
Pred. No. 48;
3; Mismatches
                                                                                                                                                                                                                                                                               Signal;
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                                                                                                            Length
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RESULT 14
Q75MC
Q75MC
ID Q75MC
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DT 05-JU
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OS Homo
OC Eukas
OC Mamma
OC NCBI
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05-JUL-2004
05-JUL-2004
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EMBL; M17278; AAC98395.
EMBL; M17279; AAC98395.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-87274906; PubMed=3038460;
Indik Z., Yoon K., Morrow S.D., Cicila G., Rosenbloom J.,
Rosenbloom J., Ornstein-Goldstein N.;
Rosenbloom J., Ornstein-Goldstein N.;
Ritructure of the 3' region of the human elastin gene: great abundance
of Alu repetitive sequences and few coding sequences.";
Connect. Tissue Res. 16:197-211(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                          Hypothetical
                                                                                                                                                                                                                          Q75MU5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001451; Hexapep_transf.
InterPro; IPR003979; tropoelastin.
PRINTS; PR01500; TROPOELASTIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analysis of cloned genomic and complementary DNA
Proc. Natl. Acad. Sci. U.S.A. 84:5680-5684(1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                         Name=ELN
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EMBL; M19265; AAC98395.1; JOINED.
EMBL; M17266; AAC98395.1; JOINED.
EMBL; M17268; AAC98395.1; JOINED.
EMBL; M17268; AAC98395.1; JOINED.
EMBL; M17270; AAC98395.1; JOINED.
EMBL; M17271; AAC98395.1; JOINED.
EMBL; M17272; AAC98395.1; JOINED.
EMBL; M17273; AAC98395.1; JOINED.
EMBL; M17274; AAC98395.1; JOINED.
EMBL; M17276; AAC98395.1; JOINED.
EMBL; M17276; AAC98395.1; JOINED.
EMBL; M17276; AAC98395.1; JOINED.
EMBL; M17278; AAC98395.1; JOINED.
EMBL; M17278; AAC98395.1; JOINED.
EMBL; M17278; AAC98395.1; JOINED.
EMBL; M17279; AAC98395.1; JOINED.
EMBL; M17278; AAC98395.1; JOINED.
EMBL; M17280; AAC98395.1; JOINED.
EMBL; M17278; FAC98395.1; JOINED.
EMBL; M172781; FAC98395.1; JOINED.
EMBL; M17279; FAC98395.1; JOINED.
EMBL; M17279; FAC98395.1; JOINED.
EMBL; M17279
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                                                                                                    domo sapiens (Human)
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
757 AA; 66136 MW; 23B7FE5B8AF85CA8 CR
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AQAAAAKAAKYGVGTPAAAAKAAAKAA 469
                                                                                                                                                              (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                          protein
                                                         Chordata;
Primates;
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Pred. No. 49;
3; Mismatches
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                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT 15
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Nature 424:157-164(2003).
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Best Local &
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05-JUL-2004
05-JUL-2004
                         PubMed=14704707; DOI=10.1038/nbt923;
Larimer F. W., Chain P., Hauser L., Lamerdin J.E., Malfatti
Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F
Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., E
Harrison F.H., Gibson J., Harwood C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-2004) to the EMBL/GenBank/DDBJ data EMBL; AC005056; AAS07435.1; -. GO:0005578; C:extracellular matrix (sensu Meta GO; GO:0005201; F:extracellular matrix structural InterPro; IPR001451; Hexapep_transf. InterPro; IPR003979; tropoelastin.
                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CGA009 / ATCC BAA-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical SEQUENCE 79
                                                                                                                                                                                                                                                                        Bradyrhizobiaceae;
                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Alphaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=RPA3180;
                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6N503;
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Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin
                                                                                                                                                                                                                                        NCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                                                           Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01500; TROPOELASTIN.
PROSITE; PS00101; HEXAPEP TRANSFERASES; UNKNOWN_1.
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Complete genome sequence
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Layman D., Maas J., Jaeger S., Walker R.,
Becker M.C., O'Laughlin M.D., Schaller M.E.,
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  the metabolically versatile
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I Nat. Biotechnol. 22:55-61(2004).

R EMBL, BiS772603; CAREMS621.1; -

R GO; GO:000786; C:nucleosome; IEA.

R GO; GO:0005634; C:nucleosome; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:000367; P:nucleosome assembly; IEA.

R InterPro; IPR005819; Histone H5.

R InterPro; IPR005819; Histone H5.

R PRINTS; PR00624; HISTONEH5.

R Complete proteome; Hypothetical protein.

Q SEQUENCE 105 AA; 11042 MW; CEDBS9B3D937E980 CRC64;
                                                                                                                                                                                                                                          GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
GO; GO:0015078; F:hydrogen ion transporter activity; IEA.
GO: GO:0016820; F:hydrolase activity, acting on acid anhydrid. .; IEA.
GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
GO; GO:0015992; P:proton transport; IEA.
InterPro; IPR002146; ATPsynt_B/B'sub.
Pfam; PF00430; ATP-synt B; 1.
CF(0); Complete proteome; Hydrogen ion transport; Ion transport;
Transmembrane; Transport.
SEQUENCE 177 AA; 18465 MW; 6F0A2E32CC3D2912 CRC64;
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Q9AB65;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ATP synthase F0, B' subunit.
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MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;

Nierman W.C., Feldeblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

DeBoy R.T., Dodson R.J., Tran K., Wolf A.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-!- SIMILARITY: Belongs to the ATPase B chain family.
EMBL; AE005710; AAK22353.1; -.
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ASAEAAERQAKEEAVLAEKLAAAEA
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ilarity 60.0%;
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SEQUENCE
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EMBL; BX248357; CAE49808.1; -
InterPro; IPR000064; NLP_P60.
Pfam; PF00677; NLPC_P60; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang P., Yang C., Sale W.S.;
"Flagellar radial spoke protein 2 is a required for motility in Chlamydomonas Bukaryotic Cell 3:72-81(2004).
EMBL; AY373262; AAQ92371.1;
InterPro; IPR007858; Dpy-30.
                                                                                                                       Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
                                                                                                                                                                                                                                                                              Q8NIZO;
01-OCT-2002
                                                                                                                                                                                              Name=5F3.190;
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                        Nyakatura
                                          Schulte
                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                Related to kinetoplast.
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PubMed=14871938; DOI=10.1128/EC.3.1.72-81.2004;
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3., Mewes F
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                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77362 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.1%;
62.5%;
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56.0%;
Hoheisel J., Brandt P., Fartmann B
H.W., Mannhaupt G.;
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27,
27,
                                                                                                                                                                                                                Last sequence update)
Last annotation update)
ciated protein KAP.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ن</u>
                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506811B4975539AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                              Sordariomycetes;
Neurospora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                          .
B.
                                            Holland
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RESULT 22
Q89IE4
ID Q89IE
AC Q89IE
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Q7PNQ9
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                                                                                                                                                                                                                                Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0004815; F:aspartate-thirling; IEA.
GO; GO:0005524; F:ANTP binding; IEA.
GO; GO:0005524; F:ANTP binding; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0006422; P:aspartyl-tran aminoacylation; IEA.
InterPro; IPR00423; Asps arch.
InterPro; IPR004364; KRNA-synt_2.
InterPro; IPR004364; KRNA-synt_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2004 (TIEMBLIEL 26,
01-MAR-2004 (TIEMBLIEL 26,
01-MAR-2004 (TIEMBLIEL 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German Neurospora genome project;
Submitted (JUN-2002) to the EMBL/
EMBL; AL807371; CAD37020.1; --
HSSP; P42639; 1C1G.
SEQUENCE 899 AA; 99309 MW; 5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50862; AA
                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004365;
InterPro; IPR006195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AAAB01008960; EAA11760.2; -.
HSSP; P04802; IASZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles gambiae str.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=ENSANGG00000015123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENSANGP00000017612 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7PNQ9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary data
                                                                                                                                                                                                                                                                                                                                                                                                                                  rPro; IPR002312; tRNA-synt_asp.
rPro; IPR004355; tRNA anti.
rPro; IPR006195; tRNA-ligase_II.
pP00122; tRNA-synt_2; 1.
pP01336; tRNA_anti; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                              l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                    PR01042; TRNASYNTHASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                 AXAEA-AEKAAKYAAEAAEKAAK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAAEEAAKKAAEEAEKARK 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAAEKAAKYAAEAAEKAAK
                                                                                                                                   TIGR00458;
                                                                                                                                                                                                                                                                                                                           531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                           58958 MW; A9468D3F53448317
                                                                                                                                                                                                                                                                                                                                                               aspS_arch; 1.
_TRNA_LIGASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%;
73.7%;
                                                                                                                                                                                                                                                    56.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                    Score 59.5;
Pred. No. 4
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                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
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                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                         Length 531;
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Q89IE4; Q89IE4;

PRELIMINARY;

PRT;

647

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RESULT

OF STATE OF S
Warrender Hopwood D.A.;

"Complete genome sequence of the mousair Complete and 1:141-147(2002).

L Nature 417:141-147(2002).

L Nature 417:141-147(2002).

L EMBL, AL939118, CAB56389.1; -.

R GO; GO:0004222; F:metalloendopeptidase activity; IF GO; GO:0006508; P:proteolysis and peptidolysis; IE; InterPro; IPR002886; Peptidase M23B.

ThierPro; IPR011054; Rudmut hyb motif.
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Best Local S
Matches 16
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01-MAY-2000
01-MAY-2000
01-MAR-2004
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01-JUN-2003
01-OCT-2003
Bll5695 prot
                                                                                                                                                                                                                                                                                                                                                               Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.
Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Marren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probable peptidase. ORFNames=SCD17.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor. Bacteria; Actinobacteria;
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DNA Res. 9:189-197(2002).
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NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=A3(2) / M145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
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nabe A., Idesawa K., Iriguca.
Shimpo S., Tsuruoka H
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K., Iriguchi M., Kawas
Tuloka H., Wada T
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STRAIN-Berkeley;
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao (
George R., Gonzalez M., Sunco J., Pacleb J., Paragas V., Par
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Par

Dhomanenavong S., Wan K., Yu C., Lewis S.E., Rubin G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35432 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tropomyosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17,
17,
26,
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26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation updat
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 43;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B4032F2A2FD9E94B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456DFC61B6C2FF0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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ra; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                   Pterygota;
                                                           iao G.,
Park S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kapur V.;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adamstides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlew R.M., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Barlew R.M., Basu A., Baxendale J., Helt G., Nelson C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Neuck J.,
RA Harris N.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Dalaz C. Davis R., Nelson K.A., Nixon K., Nusskern D., R., Pacie M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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Pfam; PF00018; SH3 1; 1.
Pfam; PF0001415; ANKYRIN.
ProDom; PD000066; SH3; 1.
SMART; SM00248; ANK; 2.
SMART; SM00326; SH3; 1.
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Q9W2J2;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=CG18375;
Drosophila melanogaster (Fruit fly).
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01-MAR-2004
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SEQUENCE
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PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0034606;
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L; BT003215; AAO24970.1;
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1020 AA; 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.2%;
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22,
26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases.
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   Reese M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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"The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                     ProDom; PD000066; SH3; 1.
SMART; SM00248; ANK; 2.
SMART; SM00326; SH3; 1.
PROSITE; PS50088; ANK REPEAT; 2.
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Patel S., Frise E., Wheeler D.A., Lewis
Ashburner M., Celniker S.E.,
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E
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EMBL; AE003453; AAF46699.3;
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Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Ra Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,
Ra Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
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Ra Liu K., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Ra Liu K., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Ra Mculov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Ra Mcunt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ra Mclson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ra Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
Ra Syirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
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Williams S.M., Woodaget, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Ra Milliams S.M., Woodaget, Worley K.C., Wu D., Zhong L.,
Ra Zheng X.H., Zhong P.N., Zhan M., Zhu S., Zhu X., Smith H.O.,
Ra Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
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A Andans M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
A Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards G., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
A Barlew R.M., Baster T. B.G., Helt G., Nelson C.R., Gabor G.L.,
A Ballew R.M., Baster B.G., Bayraktaroglu L., Beasley E.M.,
B Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
B Bellew R.M., Bernan B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
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A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
A Codson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
Changelista C.C., Ferraz C., Ferraz C., Fleischmann W.,
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                              Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G. Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubi "Finishing a whole-genome shotgun: Release 3 of the Dros
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                              ton G.G., Venter (
, Rubin G.M.;
e Drosophila
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                                                                                                                                                                                                                                                      Halpern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith H.O.
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RESULT 28
Q64SR
ID Q64SR
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Best Local
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                                                                                                                                                                                                                                                                                                                             PROSITE; PS50088; ANK REPEAT; 2.
PROSITE; PS50297; ANK REP REGION;
PROSITE; PS50002; SH3; 1.
ANK repeat; SH3 domain.
SEQUENCE 1069 AA; 115158 MW; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome
                                                                                        25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 30S ribosomal protein S16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Annotation of the Drosophila melanogaster euchromatic systematic review.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misra S., Crosby M.A., Mungail C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                              ORFNames=BF2716;
                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00248; ANK; 2.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0034606; CG18375.
InterPro; IPR002110; ANK.
InterPro; IPR001452; SH3.
                       NCBI_TaxID=817;
                                       Bacteroidaceae;
                                                    Bacteria; Bacteroidetes; Bacteroides
                                                               Bacteroides fragilis
                                                                                                                                             Q64SR3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patel S., Frise E., Wheeler
Ashburner M., Celniker S.E.;
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  SEQUENCE
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enome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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TS; PR01415; ANKYRIN.
om; PD000066; SH3; 1.
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                                                                                                                                                                                                                                                                                          Similarity
 FROM N.A.
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                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                           PRELIMINARY;
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                                       Bacteroides
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Wheeler D.A., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                        56.2%;
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                                                                                                                                                                                                                                                                                                                               115158 MW; BF102B0C044F80DA CRC64;
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                                                                                                                                                                                                                                                                                        Score 59; DB Pred. No. 97;
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                                                    (class); Bacteroidales;
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SEQUENCE FROM N.A.

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RESULT Q9VGD2
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                                                                                                                                         Q9VGD2;
Q9VGD2;
01-MAY-2000
01-OCT-2002
01-MAR-2004
CG31361-PB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VQW6
Q8VQW6;
01-MAR-2002
01-MAR-2002
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PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
4Fe-4S; Iron; Iron-sulfur; Metal-binding.
COCURNCE 496 AA; 52171 MW; 0F153E1B8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016020; C:membrane; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:00065118; P:electron transport; IEA.
Pfam; PF01512; Complex1 51K; 1.
Pfam; PF00037; Fer4; 2.
TIGREPAMS; TIGR01945; rnfC; 1.
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               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hzaapoda;
Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rubio L.M., Brown C.S., Ludden Submitted (NOV-2001) to the EME
                                                                                                                          ORFNames=CG31361;
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181 AA;
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Pred. No. 60;
4; Mismatches
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Pred. No. 26;
5; Mismatches
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                                                       Brachycera;
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Jalali M., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA, Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA, Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA, McRulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA McInco S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Rainert K., Ramington K., Saunders R.D., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Yein R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Thong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Grience 237.7185.7185.7206(2)001
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A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Barandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
A Barandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
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A Barandon R.C., Rogers Y.H., Blazej R.G., Holt G., Nelson C.R., Gabor G.L.,
A Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
A Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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                                                                MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Settencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                 a genomics
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Ashburner M., Celniker
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                     "Annotation of the Drosophila melanogaster euchromatic genome:
                                                Lewis S.E.;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
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RA Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Beason K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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RA Borkova D., Bocchan M.R., Bouck J., Brokstein P., Brottier P.,
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D. M., Nelson K.A.,
RA Roller K., Remisgon J., Sheeler F., Shen H.,
RA Roller K., Remos I., Simbson M., Skuuski M., P., Smith T.,
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SMART; SM00408; IGC2; 1.
SMOSITE; PS50835; IG LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong M., Zhang G., Zhu S., Zhu X., Smith H. Gibbs R.A., Myers E. W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirekas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Vente Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003694; AAF54750.2; IntAct; Q9VGD3; -.
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"The transposable elements of the a genomics perspective.";
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Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22426070; PubMed=12537573;
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343
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                                                                                                      4.
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                                                                                                   Score 58.5; I
Pred. No. 75;
4; Mismatches
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RESULT 32 Q8SWT7 ID Q8SWT

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InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; I.
SWART; SW00408; IGc2; 1.
PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 694 AA; 75164 MW;
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                                                                                                                                                EMBL; AL390189; CAB99171.1; -. GO; GO:0005737; C:cytoplasm; IEA. GO; GO:0016020; C:membrane; IEA. GO; GO:0008565; F:protein transporter GO; GO:0006886; P:intracellular protei
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                                                                                                                                                                                                                                                                            German Neurospora genome project;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SCHULTE U., Aign V., Hoheisel J., Brandt P., I
SCHULTE G., Mewes H.W., Mannhaupt G.;

Nyakatura G., Mewes H.W., Mannhaupt G.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurospora crassa.

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; Q9UQH9; 1E00.
FlyBase; FBgn0051361; CG31361.
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                  InterPro; IPR008938; ARM.
InterPro; IPR00695; U801_p115 C.
InterPro; IPR006953; U801_p115 head.
Pfam; PF04871; U801_p115 C; 1.
Pfam; PF04869; U801_p115 head; 1.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Drosophila melanogaster (Fruit fly).
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01-JUN-2002
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131632 MW;
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Pred. No. 78;
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protein transport;
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annotation update)
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Park S.,
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RESULT 35
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Best Local
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Q9DF23;
01-MAR-2001
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Q7V6K8;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Skin-type antifreeze polypeptide AFP-2.
Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
Cottoidei; Cottidae; Myoxocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000104; Antifreeze_1.
InterPro; IPR001778; POA_allergen_C.
InterPro; IPR001859; Ribosomal_P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98389738; PubMed=9722537; DOI=10.1074/jbc.273.36.23098; Low W.-K., Miao M., Ewart K.V., Yang D.S.C., Fletcher G.L., Hew "Skin-type antifreeze protein from the shorthorn sculpin, Myoxocephalus scorpius. Expression and characterization of a Mr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Skin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00308; ANTIFREEZEI.
PR00833; POAALLERGEN.
PR00456; RIBOSOMALP2.
E 92 AA; 7693 MW; I
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                         AXAEAAEKAAKYAAEAAEKAAKAXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chem. 273:23098-23103(1998).
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                                                                                                                                                                                                                                                                                        AAAKAAEAAAMAAANAAEAAATKAA
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he EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                   Score 58;
Pred. No.
3; Mismatc
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sequence up

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Type I antifreeze protein. OrderedLocusNames=PMT1149;

Prochlorococcus marinus

(strain

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Best Local S
Matches 19
                       EMBL; AE001367; AAC71797.2; -. PIR; A71625; A71625.
InterPro; IPR011038; Calycin.
InterPro; IPR006373; Rifin.
InterPro; IPR006373; Rifin STEVOR.
Pfam; PF02009; Rifin STEVOR; 1.
TIGRFAMs; TIGR01477; RIFIN; 1.
                                                                                                                                                                                                                                                                                                            MEDIINE-22255705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Frairlamb A.H., Fraundolz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINB-99021743; PubMed-9804551; DOI=10.1126/science.282.5391.1126;
Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
"Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947; ROCap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P., Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb E.A., Zinser E.R., Chisholm S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             096113;
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   Nature 419:498-511(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36
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19; Conserv
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  42873 MW;
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Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58;
Pred. No.
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98846A6E588C2A35 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., A. A. Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Ra Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Ra Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., A. Schitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Ra Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Ra Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Rogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., Rasmussen C., Catcheside D., Li W., Pratt R.J., Osmani S.A., Racino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., Racino G., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 13; Conserv
                        HSSP; Q33097; 1144S.

GO; GO:0005737; C:Cytoplasm; IEA.
GO; GO:0005737; E:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016874; F:proline-tRNA ligase activity; I
GO; GO:0006423; P:proly1-tRNA aminoacylation; IEA.
GO:00006423; P:proterin biosynthesis; IEA.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR002314; tRNA-synt_Dro.
InterPro; IPR002316; tRNA-synt_Dro.
InterPro; IPR002316; tRNA-synt_Dro.
InterPro; IPR006195; tRNA-synt_Dro.
InterPro; IPR006195; tRNA-synt_Dro.
IPR0129; HGTP_anticodon; I.
Pfam; PF03129; HGTP_anticodon; I.
Pfam; PF00597; tRNA-synt_Dro.
PRINTS; PR01046; TRNASYNTHPRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (2)
SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., F.
Schulte U., Aign V., Mannhaupt G.;
Nyakatura G., Mewes H.W., Mannhaupt G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Cordariomycetidae; Sordariales; Sordariaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sanotation update)
Hypothetical protein (Probable proline-tRNA ligase)
Name=NCU04449.1; Synonyms=G21B4.130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=OR74A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7RWB7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7RWB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AABX01000782; EAA26671.1; EMBL; BX908808; CAF05998.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          German Neurospora genome project;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ whole genome
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Pred. No. 56;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            shotgun
                                                                                                                                                                                                                                                                                                                                                                        activity; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Medin N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Wong A.C., Shevchenko Y., Bouffard G.G.,
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         EMBL; BC057706; AAH57706.1; -.
GO; GO:0005634; C:nucleus; IEA,
GO; GO:0003676; F:nucleus acid binding; IEA,
GO; GO:0003700; F:transcription factor activity;
GO; GO:0003755; P:regulation of transcription, DN
InterPro; IPR003007; Pept Aspartic.
InterPro; IPR003309; Treg_SCAN.
InterPro; IPR001878; Znf_CCHC.
DSGM. PEONO3339; Treg_SCAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TREMBLrel. 27, Created)
05-JUL-2004 (TREMBLrel. 27, Last sequence update)
05-JUL-2004 (TREMBLrel. 27, Last annotation update)
05-JUL-2004 (TREMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Hypothetical protein; Ligase.
SEQUENCE 558 AA; 63124 MW; 95E5E653
                                                                                                                                                               Klein S., Strausberg R.;
Submitted (SEP-2003) to
                                                                                                                                                                                                                                                                                                                Richardson P
                                                                                                                                                                                                                                                                                                                              Klein S.L., Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Generation and initial analysis and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., But Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A.,
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                                                                                                                                                                                                     TISSUE=Embryo;
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22341132;
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                                                                                                                                                                                                                                                                            initiative
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones S.J., Marra M.A.;
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                                                                                                                                                                                                                      FROM N.A.
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                                                                                                                                                                                                                                                           225:384-391 (2002) .
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                                                                                                                                                                                                                                                                                           genomic tools for Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus.
                                                                                                                                                                                                                                                                                                                              PubMed=12454917; DOI=10.1002/dvdy.10174;
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59.1%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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75;
                                                                                                                                                                                                                                                                                             research: The NIH Xenopus
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                                                                        DNA-dependent; IEA.
                                                                                            IEA.
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RESULT 40
P90534
ID P9053
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DT 01-MA
DT 01-MA
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Lactobacillus plantarum WCFS1.", Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
-i- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AL935253; CAD63322.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=NCIMB 8826 / WCFS1;
MEDLINE=22480296; Pubmed=12566566; DOI=10.1073/pnas.0337704100;
Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursin
De Vos W.M., Siezen R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00005; ABC_tran; 2,
ProDom; PD000006; ABC_transporter; 2,
SMARF; SM00382; AAA; 2.
SMARF; PS50893; ABC_TRANSPORTER_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0042626; F:ATPase activity, cou
GO; GO:0000166; F:nucleotide binding;
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactobacillus.
NCBI_TaxID=1590;
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01-JUN-2003 (TrEMBLrel. 24, I
01-MAR-2004 (TrEMBLrel. 26, I
ABC transporter, ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Co
SEQUENCE 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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InterPro; IPR003439; ABC transpo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P58301; 1US8.
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                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                   EQAETAAAAASQAAEKAAEAGA
                                                                                                                                                                                                                                 EAAEKAAKYAAEAAEKAAKAXA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 1
575 AA; 62786 MW;
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                                                                                                                                                                                                                                                                                                                                                                                             Complete
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                                                                                                                                                                                                                                                                                                                                                                       74176 MW;
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63.6%;
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                                                                                                                                                                                                                                                                                                   Score 58;
Pred. No.
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                                                                                                                                                                                                                                                                                                        86;
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P90534; P90534; 01-MAY-1997 01-MAY-1997

(TrEMBLrel. 03, (TrEMBLrel. 03, PRELIMINARY;

Last Created)

sequence update)

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POLI TORVE STANDARD; PRT; 2197 AA.

POLI TORVE STANDARD; PRT; 2197 AA.

POLI TORVE STANDARD; PRT; 2197 AA.

POLITORY STANDARD; PRT; 2197 AA.

POLITOR STANDARD; PRT; 2197 AA.

PRT; 2197 AA.

POLITOR STANDARD; PRT; 2197 AA.

POLITOR STANDARD STANDAR
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GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport;
InterPro; IPR008160; Collagen.
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Submitted (DEC-1996) to the
EMBL; U83087; AAB40930.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ptam;
"Proteolytic processing of tomato ringspot precursors: definition of the domains for t putative RNA-dependent RNA polymerase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rott M.E., Tremaine J.H., Rochon D.M.; "Comparison of the 5' and 3' termini of RNA2: evidence for RNA recombination."; Virology 185:468-472(1991).
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                                                                                                                       Wang A., Car
Sanfacon H.;
                                                                                                                                                                                                            PubMed=10092022;
                                                                                                                                                                                                                                                      SEQUENCE OF 1213-1247
MUTAGENESIS OF GLN-14
                                                                                                                                                                                                                                                                                                                                                                                                               Hans F., Sanfacon H.;
"Tomato ringspot nepovirus
site specificity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9049338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95146991; PubMed=7844569;
Rott M.E., Gilchrist A., Lee L., Rochon D.M.;
"Nucleotide sequence of tomato ringspot virus RNA1.";
J. Gen. Virol. 76:465-473(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand
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                                                                                                                                                                     Carrier K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                              13-1247 AND 1487-1502,
GLN-1465 AND GLN-1486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collagen; 1.
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                                                                                                                                                                 Chisholm J., Wieczorek A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pum (Slime mold).
Dictyosteliida; Dictyostelium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
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        for the .";
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the VPg, protease and
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                                                                                                                                                                                                                                                                                            POLYPROTEIN,
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InterPro; IPR004004; Pept_Calici.
InterPro; IPR010464; Picornain 3C.
InterPro; IPR0010605; RNA_helicase.
InterPro; IPR007095; RNA_pol_DS PS.
InterPro; IPR0071095; RNA_pol_DS PS.
InterPro; IPR0071094; RNA_pol_PSvir.
Pfam; PP00643; Picornain 3C; 1.
Pfam; PP00680; RNA_dep_RNA_pol; 1.
Pfam; PP00680; RNA_dep_RNA_pol; 1.
Pfam; PP00910; RNA_helicase; 1.
                                                                                                                                                                           EMBL; L19655; AAA78254.1; -
EMBL; M73822; AAA47942.1; -
EMBL; M38822; AAA47942.1; A
PIR; A40787; GNVVSR.
MEROPS; C03.012; -
                                                                                              InterPro; IPR004004; I
InterPro; IPR010464; I
InterPro; IPR000605;
InterPro; IPR007095; I
InterPro; IPR001205; I
InterPro; IPR001205; I
PRINTS; PR00918; CALICVIRUSNS.
ATP-binding; Covalent protein-RNA linkage; Direct protein Glycoprotein; Hydrolase; Polyprotein; Protease; PMA-directed RNA polymerase; Thiol protease; Transferase;
                                                                                                                                                                                                                                                                   "Tomato ringspot virus proteins containing the nucleoside triphosphate binding domain are transmembrane proteins that associate with the endoplasmic reticulum and cofractionate with replication complexes.";
                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION OF THE NBT-VPG PROTEIN. PubMed=12477857; DOI=10.1128/JVI.77.1.523-534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang A., Sanfacon H.; "Proteolytic processi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang A., Han S., Sanfacon H.;
"Topogenesis in membranes of the NTB-VPg
                                                                                                                                                                                                                                                             or send
                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nepovirus: definition of the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=14769910; DOI=10.1099/vir.0.19612-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY
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- SIMILARITY:
- SIMILARITY:
- CAUTION: It
                                                                                                                                                                                                                                                                                                                                                                                                                                                             is an integral membrane protein.
PTM: Specific enzymatic cleavages by 3C-like protease in vivo yield mature proteins. 3C-like protease is autocatalytically processed. NBT exists as NBT-VPg polyprotein as well as NBT mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: The NTB-endoplasmic-derived membranes
                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
PTM: VPg is covalently linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: The NTB-VPg polyprotein endoplasmic-derived membranes that are active replication. VPg localizes to the endoplasmic
                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                     initiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RNA) (N)
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                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                  Belongs to the nepoviruses RNA1 polyprotein Contains 1 peptidase C3 domain. is uncertain whether Met-1 or Met-122 is the
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                                                                                                                                                                                                       ALT_INIT
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                                 sequencing;
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        InterPro;
PROSITE; I
Complete I
                                                                                        MEDLINE-22404998; PubMed-12597275;

Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,

Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,

Sobara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada
                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
CHAIN
CHAIN
                                   Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
                                                                                                                                                               Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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DOMAIN
                                                                                                                                SEQUENCE FROM N.A. STRAIN=USDA110;
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                                                                                                                                                                                               OrderedLocusNames=bll5696;
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                        L; AP005955; BACS0961.1;
GO:0030693; F:caspase activity;
GO:0006508; P:proteolysis and peerPro; IPR001309; ICE_P20.
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H-D: Complete loss of protease activity.
H-L: Complete loss of protease activity.
Q->A: No effect.
Q->A: No cleavage between 3C-like protease and RNA-directed RNA polymerase.
T-> A (in Ref. 4; AA sequence).
8 MW; 2D8EF928E58DBC89 CRC64;
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3C-like protease (Probable 3C-like protease (Potentia 3C-like protease (Potentia Involved in the cleavage s
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No cleavage between X2
No cleavage NTB and VR
mplete loss of N-linked
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2.3e+02;
5;
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                                                             STRAIN-0157:H7 / BDL933 / ATCC 700927 / EHBC;
STRAIN-0157:H7 / BDL933 / DOI:10.1038/35054089;
MEDLINE=21074935; PubMed=11206551; DOI:10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
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SEQUENCE
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01-MAR-2002 (TrEMBLrel. 20, Last
25-OCT-2004 (TrEMBLrel. 28, Last
Membrane spanning protein, requir
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"Limited sequence polymorphism in
surface protein 3.",
Mol. Biochem. Parasitol. 87:231-23
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SEQUENCE FROM N.A.
MEDLINE=97391128; PubMed=9247935; DOI=10.1016/S0166-6851(97)00067-4;
Huber W., Felger I., Matile H., Lipps H.J., Steiger S., Beck H.P.;
Huber W., Fender Folymorphism in the Plasmodium falciparum merozoite
                                                                                                                                                                                                                                                                                                                                                                                               (Membrane spanning protein TolA).
Name=tolA; OrderedLocusNames=ECs0774,
Escherichia coli 0157:H7.
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Eukaryota; Alveolata;
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01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2004 (TrEMBLrel. 26,
Merozoite surface protein 3
                                                                                                                                                                                                                                                                                   SEQUENCE
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                                         Nature 409:529-533(2001)
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AF001149; AAC47674.1; -.
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Last sequence update)
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(Fragment).
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Page 20

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RESULT 45
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Pfam; PF00515; TPR I; 1.
SMART; SM00271; DnaJ; 1.
SMART; SM00028; TPR; 3.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS50005; TPR; 2.
PROSITE; PS50005; TPR, REGION; 1.
Kinase; Repeat; TPR repeat.
SEQUENCE 508 AA; 55747 MW; 5826AC06E1E8DB9C CRC64;
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX088700; CAD60707.1; -.
HSSP; P08622; 1BQZ.
GG; GG:0016301; F: kinase activity; IEA.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR008940; Prenyl_trans.
InterPro; IPR001840; TPR.
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Q875A8;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

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"Complete genome sequence of enterohemorrhagic Escherichia coli

0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
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PIR; G95576; G85576.
HSSP; P19934; 1TOL.
InterPro; IPR010528; TolA.
Pfam; PF06519; TolA; 1.
Complete proteome.
Complete 394 AA; 40517 MW; 5B58D8E8230BDE28 CRC64;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
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                                                                                                                                                Local Similarity
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136 AAVEAAKAAAKAAEAAAKAG 155
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                                                                                                                                             54.3%; Score 57; 70.0%; Pred. No.
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Search completed: July 11, Job time : 170 secs

2005, 09:46:25

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Run on:
                                                                                                   OM protein - protein search, using sw model
July 11, 2005, 09:22:59; Search time 161 Seconds (without alignments) 60.056 Million cell updates/sec
                                                                                                                                                                             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compus
                                                                                                                                                                                  Compugen Ltd.
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Title: Sequence: Perfect score: SEQ1 1 axaeaaekaakyaaeaaekaakaxa 25

Scoring table: BLOSUM62DX Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues

Searched:

Total number of hits satisfying chosen parameters: 2105692

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database A\_Geneseq\_16Dec04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003bs:\*
7: geneseqp2003bs:\*
8: geneseqp2004s:\*

Pred. No. is the score greater the and is derived by is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

#### SUMMARIES

25	24	23	22	21	. 20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4	w	N	1	Result
63	63	63	63	63	63.5	63.5	63.5	63.5	64	64	64	64	64	64	64	64	64	64	65.5	67	67	67	67	105	Score
60.0	60.0	60.0		60.0	60.5	60.5	60.5	60.5	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0	61.0		63.8	63.8	63.8	63.8	100.0	Query Match
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ADE10697	ADK15667	ADK15717	ADE10648	ADE10698	ADK15653	ADK15703	ADE10634	ADE10684	ADK15651	ADK15702	ADK15701	ADK15652	ADE10632	ADE10633	ADE10682	ADE10683	ADO43177	ADO43180	ABU27824	ADK15704	ADK15654	ADE10635	ADE10685	AAB66787	ID
Ade10697 Structura	Adk15667 Nucleatin	Adk15717 Library f	Adel0648 Structura	Adel0698 Structura	Adk15653 Nucleatin	Adk15703 Library f	Adel0634 Structura	Adel0684 Structura	Adk15651 Nucleatin	Adk15702 Library f	Adk15701 Library f	Adk15652 Nucleatin	Adel0632 Structura	Adel0633 Structura	Ade10682 Structura	Adel0683 Structura	Ado43177 Peptide u	Ado43180 Peptide u	Abu27824 Protein e	Adk15704 Library f	Adk15654 Nucleatin	Adel0635 Structura	Ade10685 Structura	phipa	Description

45	44	43	42	41	40	39	38	37	36	35	34	<u>ყ</u>	32	31	30	29	28	27	26
63	63	63	63	63	63	63	63	63	63	63	63	63	<u></u>	63	63	63	63	63	63
60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0
104	91	91	91	91	88	88	88	88	83	83	83	83	75	75	75	75	67	67	67
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ADE10690	ADK15713	ADK15663	ADE10644	ADE10694	ADK15661	ADK15711	ADE10692	ADE10642	ADK15664	ADK15714	ADE10645	ADE10695	ADK15665	ADK15715	ADE10646	ADE10696	ADK15716	ADK15666	ADE10647
Ade10690	Adk15713	Adk15663	Ade10644	Ade10694	Adk15661	Adk15711	Ade10692	Ade10642	Adk15664	Adk15714	Ade10645	Ade10695	Adk15665	Adk15715	Ade10646	Ade10696	Adk15716	Adk15666	Adel064/
Structura	Library t	Nucleatin	Structura	Structura	Nucleatin	Library t	Structura	Structura	Nucleatin	Library 1	Structura	Structura	Nucleatin	Library f	Structura	Structura	Library t	Nucleatin	structura

# RESULT 1 AAB66787 ID AAB6 XX AC AAB6 XX AAB66787 standard; peptide; 25 Ä

ALIGNMENTS

AAB66787;

11-APR-2001

(first entry)

Amphipathic peptide conjugate

Amphipathic; lipid bilayer; detergent.

Synthetic.

WO200102425-A2

11-JAN-2001.

29-JUN-2000; 2000WO-CA000773

29-JUN-1999; 99US-0140988P

(UYHE-) UNIV HEALTH NETWORK.

Prive G;

WPI; 2001-138120/14.

New amphiphatic peptide conjugate having detergent properties, and hydrophobic and hydrophilic phase, useful e.g. for stabilizing and crystallizing proteins and membrane proteins, as cytolytic agents, surfactants or emulsifiers.

Claim 1; Page 22; 29pp; English.

The present invention relates to an amphipathic peptide conjugate having detergent properties and a hydrophobic and hydrophilic face. The amphipathic peptide conjugate may be used for the stabilization and crystallization of proteins and membrane proteins, for modifying the properties of lipid bilayer membranes, as cytolytic agents, as molecules that can facilitate the transport of polar molecules across biological membranes, and as emulsifiers and surfactants

Sequence 25 AA;

Query Match 100.0%; Score 105; DB 4; Best Local Similarity 100.0%; Pred. No. 3.2e-07; Matches 25; Conservative 0; Mismatches 0; Length 25; Indels <u>.</u> Gaps 0

5

AXAEAAEKAAKYAAEAAEKAAKAXA

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                   peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be introduced into any tumour cell (primary or cultured), and peptides dientified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the brca-1 or brca-2 genes, and other tumour suppressor genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence, where N1 is fused to N2. Disclosed is a method for screening bioactive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lalpha helical biasing sequence, respectively, useful in screening
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08-OCT-1999;
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nes, and other tumour suppressor such as the adenomatous polyposi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIg; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response.
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99US-00415765.
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2; Mismatches
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The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a scaffold protein sequence; and a second nucleic acid (NI), encoding a library peptide sequence comprising an alpha helical biasing sequence;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence; nucleating sequence; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology applications, infectious disease applications, drug toxicities and drug resistance applications, immunobiology, inflammation, and allergic
                                           (ANDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleating sequence-containing library fusion protein #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK15654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 104
                                                                                                                                                                                                                                  08-OCT-1998;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003224412-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK15654 standard; peptide; 104 AA
                                                                                                                                                                                            20-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                              18-MAR-2003; 2003US-00393449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10
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                                           ANDERSON D. PEELLE B R.
    BOGENBERGER J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AXAEAAEKAAKYAAEAAEKAAKAXA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAAEAAAKAAAEAAAKAAAEAA
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99US-00415765.
2002US-00177725.
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Pred. No. 0.18;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 104 AA;
                                                            Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                                                                                                (ANDE/)
                                                                                                                                                                                                                                     08-OCT-1998;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                  fusion nucleic acid library; fusion protein library; scaffold protein;
green fluorescent protein; GFP; alpha helical biasing sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK15704 standard; peptide; 104 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson D,
                                                                                                                  WPI; 2004-033956/03.
                                                                                                                                           Anderson D,
                                                                                                                                                                                                                                                                             18-MAR-2003; 2003US-00393449
                                                                                                                                                                                                                                                                                                        04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                    nucleating sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Library fusion protein-related scaffold protein #36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK15704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; SEQ ID NO 42; 110pp; English.
                                                                                                                                                                                                                          20-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AAAAAAEAAAKAAAEAAAKAAAEAA 34
                                                                                                                                                                    ) ANDERSON D.
) PEELLE B R.
) BOGENBERGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                           Peelle BR,
                                                                                                                                                                                                                        99US-00415765
2002US-00177725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peelle BR,
                                                                                                                                                                                                                                                    98US-00169015.
                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                      screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.8%;
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                                                                                                                                           Bogenberger JM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 67; DB 8
Pred. No. 0.18;
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                                                               nucleating sequence
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The invention comprises a library of fusion encoded protein contains a scaffold protein

nucleic acids, where each (e.g. a green fluorescent

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92;

110pp; English.

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein - GFP) and a library peptide sequence comprising an alpha biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for sc bioactive peptides conferring a particular phenotype. The present acid sequence represents a scaffold protein.
                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 55748; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                                                                                                                            isolate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #13351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT-)
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                  ACA31694
                                                                                                                                                                                                                                                                                                                                          candidate molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAAAEAAKAAAEAAAKAAAEAA 34
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                                                                                                                                                                                                                                                                                                                                          for rational drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                          discovery
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Xu HH;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this
                                                                                                                                                                                             Detecting, identifying and sequencing of biomolecules using controlled alignment of nano-barcodes encoding specific information for scanning probe microscopy, useful in the fields of molecular biology.
                                                                                                                                                                                                                                                                                                                                       20-SEP-2002; 2002US-00251152.
19-SEP-2003; 2003US-00667004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nano-barcode;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADO43180 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the target prokaryotic essential genes. Note: The sequent and not form part of the printed specification, in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                       WPI; 2004-399960/37.
                                                                                                                                                                                                                                                                                Chan S,
                                                                                                                                                                                                                                                                                                                                                                                22-SEP-2003; 2003WO-US029726
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                                                                                                                                                                                                                                                                                Su X, Yamakawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEAEAAKKAAQEAEKKAAAEAAKKAAAAE 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for coded probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                             CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scanning probe microscopy; probe
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62.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthesis.
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 428;
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The present sequence is that of a peptide of potential use for production of a coded probe useful in the method of the invention. The invention provides methods, apparatus and compositions for the detection, identification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule(s). After more nano-barcodes are allowed to bind to target molecule(s). After binding and separation from unbound coded probes, the bound coded probes are aligned on a surface and analysed by scanning probe microscopy (SPM). The methods allow the sequencing of long nucleic acid sequences in a single sequencing run, high speed of obtaining sequence data, low cost of

in terms

sensitive

Example 2; Page 44; 63pp; English

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RESULT 8
ADO431177
ID ADO4
AC ADO4
AC ADO4
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                                                                                                                                    Query Match
Best Local S
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Best Local
                                                                                                                                                                                                                                                                                                                                                                               provides methods, apparatus and compositions for the detection, identification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule(s). After binding and separation from unbound coded probes, the bound coded probes are aligned on a surface and analysed by scanning probe microscopy (SPM). The methods allow the sequencing of long nucleic acid sequences in a signal acid sequences in a signal acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting, identifying and sequencing of biomolecules using controlled alignment of nano-barcodes encoding specific information for scanning probe microscopy, useful in the fields of molecular biology.
                                                                                                                                                                                                                                                                                                     single sequencing run, high speed of obtaining sequence data, sequencing and high efficiency in terms of operator time, and and accurate detection and/or identification of nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-SEP-2002; 2002US-00251152.
19-SEP-2003; 2003US-00667004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nano-barcode; scanning probe microscopy; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AD043177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and accurate detection and/or identification of nucleic acids with low incidence of false positive results.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a peptide of of a coded probe useful in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 44; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-399960/37
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                                                                                                                                                                                                                      Sequence
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                                                                                                         15;
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AAKAAAKAAKAAKAAKAA 23
                                                    XAEAAEKAAKYAAEAAEKAAKAX 24
                                                                                                                                                                                                                                                                              of false positive results.
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                                                                                                      Score 64; DB
Pred. No. 0.1;
5; Mismatches
                                                                                                                                       0.1;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; cell division; decreased cell growth; brca-1; brca-2;
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08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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99US-00415765
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Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lapha helical biasing sequence, respectively, useful in screening having and

Disclosure; SEQ ID NO 90; 110pp; English

The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology

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Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell athesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a scaffold protein used in peptide libraries ot hold the library peptide in a conformationally
                     The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where NI is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other
                                                                                                                                                                                                                                                                                                                                                                                                   Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lalpha helical biasing sequence, respectively, useful in screening
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08-OCT-1999;
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99US-00415765
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                                                                                                                                                                                                                                                                                                   89; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bogenberger JM;
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Pred. No. 0.
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CC candidate peptides and to identify target molecules, i.e., the molecules CC with which the bloactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic CC relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be CC introduced into any tumour cell (primary or cultured), and peptides CC identified which by themselves induce apoptosis, cell death, loss of cell cdivision or decreased cell growth. The method is also useful for CC screening of bloactive peptides which restore the constitutive function of the brca-1 or brca-2 genes, and other tumour suppressor genes CC (APC) and the Drosophila discs-large gene (DIg), which are components of CC ell-cell junctions. The methods are useful in cardiovascular cell-cell junctions, commeceutical applications, endocrinology applications, infectious disease applications, drug toxicities and drug resistance applications, immunobiology, inflammation, and allergic cresistance applications, and biotechnology applications. The peptide clibrary can easily be monitored, both for its presence within cells and cits quantity. The expression of structurally biased libraries generate CC elevated cellular concentration of peptides having a given structural consentration acid sequence of a scaffold protein used in ceptide libraries of hold the library peptide in a conformationally
  Query Match
                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the equilibrium state (i.e., half-life) or one or more RNAs, proteilipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more
                                                                                                             restricted form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins,
                                                      104 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytokines, or other molecules; changes
  BB
7;
  Length 104;
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밁 Ş Matches Local φ 1 AXAEAAEKAAKYAAEAAEKAAKAXA 18; Similarity AAAEAAAKAA - - AAAAAEAAAKAAA Conservative 61.0%; 2 Score Pred. Mismatches No. 31 25 0.45; ω --Indels 2; ۲.

ADE10633
ID ADE10
XX ADE10
AC ADE10
XX Struc
XX Eusic
XX fusic
XX Synth
XX Synth
XX Synth
XX Synth
XX Synth
XX 1-JU
XX 108-00
PR 08-00
PR 08-00 Structurally biased random peptide library related protein seqid 40. 29-JAN-2004 ADE10633 standard; protein; (first entry) 104 ₽

tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; Drosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmecceutical; endocrinology; infectious disease; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cel loss of cell division; decreased cell growth; brca-1; brca-2; fusion nucleic acid library; scaffold protein; bioactive toxicity; drug resistance; inflammation; allergic peptide; cell death;

Synthetic

US2003143562-A1

20-JUN-2002; 2002US-00177725

08-OCT-1998; 08-OCT-1999; 98US-00169015 99US-00415765

(RIGE-) RIGEL PHARM INC

density; changes

expression of one or more

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RESULT 12
ADE10632
ID ADE10
XX ADE10
XX ADE10
XX ADE10
XX Struc
XX Struc
XX Fusic
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention.
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phenotype change;
cell adhesion; cel
loss of cell divis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bloactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 104
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                                                                                                                     fusion nucleic acid library; scaffold protein;
                                                                                                                                                                                            Structurally
                                                                                                                                                                                                                                                                                                                                                                                                                        ADE10632 standard; protein; 104 AA
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ge; cell morphology; cell growth; cell viability;
   cellular density; cancer; tumour; apoptosis; cell death;
ivision; decreased cell growth; brca-1; brca-2;
                                                                                                                                                                                            random peptide library related protein segid 39
                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.0%;
72.0%;
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Pred. No. 0.
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                                                                                                                         bioactive
                                                                                                                     peptide;
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Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response.
                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-1998;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-2002; 2002US-00177725
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                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-829786/77.
                                                                                                                                                                                                                                                                                                                                                                                             (RIGE-) RIGEL
                                                                                                                                                                                                                                                                                                                                                                              Peelle BR,
                                                                                                                                                                                                                                                                                                                                                                                             PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                            98US-00169015.
99US-00415765.
                                                                                                                                                                                                                                                                                                                                                                              Bogenberger JM;
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Example 6; SEQ ID NO 39; 110pp; English

CC Time invention describes a library (1) or rusion nucleic acids, where each CC fusion nucleic acid (N1), encoding a CC scaffold protein sequence; and a second nucleic acid (N2), encoding a CC library peptide sequence comprising an alpha helical biasing sequence; CC where NI is fused to N2. Disclosed is a method for screening bioactive CC morphology, cell growth, cell viability, adhesion to substrates or other CC cells, and cellular density; changes in the expression of one or more CC in the equilibrium state (i.e., half-life) or one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the expression of one or more cells, proteins, cytokines, or other molecules; changes condidate peptide by above mentioned method is used to generate more CC candidate peptides and to identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic condinated with other pharmacologic activators to study the epistatic conditions in the angular transduction pathways in question. The disclosed conditions or decreased cell growth. The method is also useful for controduced into any tumour cell (primary or cultured), and peptides of important in breast cancer spelications. Random libraries can be comported by the method is also useful for controduced into by themselves induce apoptosis, cell death, loss of cell cidentified which by themselves induce apoptosis, cell death, loss of cell controduced into any tumour cell growth. The method is also useful for conformations of bioactive peptides which restore the constitutive function conformations, nearly protections, bone biology applications, skin cell cell junctions. The methods are useful in cardiovascular conformations, immunobiology, inflammation, and allergic creatories and drug creatories applications, end biotechnology applications. The peptide response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention. The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a

Matches Query Match Best Local Similarity Conservative 61.0%; 72.0%; Score 64; D. Pred. No. 0. 2; Mismatche Mismatches 멂 .45 Length 104; Indels *ي* Gaps

Sequence 104 AA;

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RESULT 13
ADK15652
ID ADK15
XX ADK15
AC ADK15
XX Nucle
XX Vucle
XX fusi
XX Syntl
XX fusi
XX Syntl
XX Syntl
XX Hoso
PR 08-00
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                                                                                                                                                                                         RESULT 14
ADK15701
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
Library fusion protein-related scaffold protein
                                                        06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1998;
08-OCT-1999;
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green fluorescent protein; GFP; alpha helical biasing sequence;
                                                                                                          ADK15701;
                                                                                                                                                             ADK15701 standard; peptide; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; SEQ ID NO 40; 110pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ANDE/) ANDERSON D. (PEEL/) PEELLE B R.
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                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
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                                                                                                                                                                                                                                                                                                                                  AXAEAAEKAAKYAAEAAEKAAKAXA 25
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AAAEAAKAA--AAAAAEAAAKAAA
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                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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99US-00415765.
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72.0%;
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Pred. No. 0.45
2; Mismatches
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RESULT 15
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Best Local Similarity
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                                                                                                                                                                                                                                 fusion nucleic acid library; fusion protein library; scaffold protein;
green fluorescent protein; GFP; alpha helical biasing sequence;
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                                         18-MAR-2003; 2003US-00393449
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                                                                                                                                                                                                                sequence;
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Pred. No. 0.45;
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Best Local
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                                                                                                                                                                                                                                                                                      green fluorescent
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20-JUN-2002; 2002US-00177725
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of fusion polypeptides in which each polypeptides comprises d protein and library peptide having alpha helical biasing e, or scaffold protein, library peptide and nucleating seque:
                                                                                                       ANDERSON D.
PEELLE B R.
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Pred. No. 0.45
2; Mismatches
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RESULT 17
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The invention describes a library (I) of fusion nucleic acids, where endusion nucleic acid comprises a first nucleic acid (NI), encoding a scaffold protein sequence; and a second nucleic acid (NI), encoding a library peptide sequence comprising an alpha helical biasing sequence; where NI is fused to NI. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmeccutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response;
                                                                                                                                                                                                                                                                                           Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening
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08-OCT-1999;
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Pred. No. 0.45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                       where each
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a scaffold protein used in peptide libraries of hold the library peptide in a conformationally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells,
                                                                                                                                                                                                                                                                                                                                                                                                                            tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; Drosophila discs-large; DIg; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structurally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules, i.e., the molecules
   08-OCT-1999;
                                 08-OCT-1998;
                                                                                                       20-JUN-2002; 2002US-00177725
                                                                                                                                                                                                                                                     US2003143562-A1
                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE10634 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 104
                                                                                                                                                                                                                                                                                                                                                                                                  toxicity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           μ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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98US-00169015.
99US-00415765.
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                                                                                                                                                                                                                                                                                                                                                                                                  resistance; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  random peptide library related protein segid 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.5%;
72.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63.5; DB Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                  allergic response
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CC morphology, cell growth, cell viability, adhesion to substrates or other CC cells, and cellular density; changes in the expression of one or more CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein, CC lipids, hormones, cytokines, or other molecules; etc. The bioactive CC peptide identified by above mentioned method is used to generate more CC candidate peptides and to identify target molecules, i.e., the molecules (can be combined with other pharmacologic activators to study the epistatic CC relationships of signal transduction pathways in question. The disclosed CC introduced into any tumour cell (primary or cultured), and peptides (cidentified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function CC of the brca-1 or brca-2 genes, and other tumour suppressor genes CC (APC) and the Drosophila discs-large gene (DIg), which are components of coll-cell junctions. The methods are useful in cardiovascular applications are useful in Cardiovascular applications.
                                           applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology applications, infectious disease applications, drug toxicities and drug resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptides conferring a change in specific phenotype such as cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; SEQ ID NO 41; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-829786/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a library (I) of fusion nucleic acids, where each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIGE-) RIGEL PHARM INC
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RESULT 19
ADK15703
ID ADK15
XX
XX
AC ADK15
XX
DT 06-MA
DT 1bra
XX
KW fusic
KW greer 맑 δ Matches Query Match Best Local : Library fusion protein-related scaffold protein #35. 06-MAY-2004 ADK15703 standard; peptide; 104 AA 18; 1 AXAEAAEKAAKYAAEAAEKAAKAXA 25 Similarity Conservative (first entry) 72.0%; Mismatches Score 63.5; Pred. No. 0 29 . 52 ; B 7; 4: Length 104; Indels ۲. Gaps ۲,

Sequence

104 AA;

fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence;

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RESULT 20
ADK15653
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Best Local S
Matches 18
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                                                                                                                                              fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence; nucleating sequence; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
          08-OCT-1999;
20-JUN-2002;
                                 08-OCT-1998;
                                                      18-MAR-2003;
                                                                              04-DEC-2003
                                                                                                    US2003224412-A1.
                                                                                                                          Synthetic
                                                                                                                                                                                            Nucleating
                                                                                                                                                                                                                    06-MAY-2004
                                                                                                                                                                                                                                           ADK15653;
                                                                                                                                                                                                                                                                 ADK15653 standard; peptide; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-033956/03.
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08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                             AAAAAEAAAK-AAAAAEAAAKAAA
                                                                                                                                                                                            sequence-containing library fusion protein #35
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99US-00415765.
2002US-00177725.
                                                       2003US-00393449.
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            2002US-00177725
                      98US-00169015.
99US-00415765.
                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                   60.5%;
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                                                                                                                                                                                                                                                                                                                                                                                               Length 104;
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RESULT 21
ADE10698
ID ADE10698
ID ADE10698
AC ADE10
XX ADE10
XX ADE10
XX Fusic
XW Fusic
XW Fusic
XW Phenc
XW Celll
XW Loose
XW Celll
XW Loose
XW Skin
XW Grose
XW Syntl
XX AC GROS
PF 20-JI
XX AC GROS
PR 08-O
XX RIG
XX ANDS
PR 08-O
XX ANDS
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PR WPI;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIg; cardiovascular; neurobiology; bone biology; skin biology; cosmecceutical; endocrinology; infectious disease; drug revisity. Arms resistance in the content of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 104 AA;
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                                                                                                                                                                                                                                                    08-OCT-1998;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                       20-JUN-2002; 2002US-00177725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2004
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                                                                                                                                                                                               (RIGE-) RIGEL
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                                                                                     2003-829786/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxicity; drug resistance; inflammation; allergic response;
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) PEELLE B R.
) BOGENBERGER .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  АХАБАЛЕКЛАКУАЛБАЛБКАЛКАХА 25
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                                                                                                                                       Peelle
                                                                                                                                                                                                  PHARM INC
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99US-00415765.
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                                                                                                                                       BR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
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                                                                                                                                       Bogenberger
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide become

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
                                                fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cell under density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmecceutical; endocrinology; infectious disease; skin biology; cosmecceutical; endocrinology; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a scaffold protein used peptide libraries ot hold the library peptide in a conformationally
                                                                                                                                                                                                                                                                      Structurally biased random peptide library related protein seqid 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive
                                                                                                                                                                                                                                                                                                                               29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE10648 standard; protein; 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restricted form.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention describes a library (I) of fusion nucleic acids, where each on nucleic acid comprises a first nucleic acid (N1), encoding a
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                                                                                                                                                                                                                                                                                                                            (first entry)
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2; Mismatches
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0.32;
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peptides conferring a change in specific phenotype such as cell composition, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more CC enlis, and cellular density; changes in the expression of one or more CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein, clipids, hormones, cytokines, or other molecules; ctc. The blocative peptide identified by above mentioned method is used to generate more CC candidate peptides and to identify target molecules, i.e., the molecules ctc. The blocative peptide interacts The peptide(s) can be cc. with which the blocative peptide interacts The peptide(s) can be cc. with which the blocative peptide interacts The peptide(s) can be cc. and the combined with other pharmacologic activators to study the epistatic crelationships of signal transduction pathways in question. The disclosed controduced into any tumour cell (primary or cultured), and peptides clidentified which by themselves induce applications. Random libraries can be cc. identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of blocative peptides which restore the constitutive function confined the Drosophila discs-large gene (DIg), which are components of coll-cell junctions. The methods are useful in cardiovascular applications beneful in cardiovascular and cardiovascular applications beneful in cardiovascular and cardiovascular applications beneful in cardiovascular and cardiovascular applications.
                                            response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention.
                                                                                                                                                                                                                                   applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology applications, infectious disease applications, drug toxicities and drug resistance applications, immunobiology, inflammation, and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scaffold protein sequence; and a second nucleic acid (N2), er library peptide sequence comprising an alpha helical biasing where N1 is fused to N2. Disclosed is a method for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1998;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a
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99US-00415765.
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Sequence 59 AA;

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                 Matches
                              Query Match
                        Local
                       Similarity
ХАЕАЛЕКАЛКУЛЛЕЛЛЕКАЛКАХА 25
                       60.0%;
                2
                       Score 63;
Pred. No.
             Pred. No. 0.3
2; Mismatches
                              DΒ
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                6,
                              Length 59
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                Gaps
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resistance; inflammation; allergic response

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ADK15717
ID ADK15
XX O6-N
XX O6-N
XX O6-N
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KW Gusi
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ADK15667
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a scaffold protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
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Synthetic
                                                fusion nucleic acid library; fusion protein library; green fluorescent protein; GFP; alpha helical biasing nucleating sequence; screening.
                                                                                                                                                       Nucleating sequence-containing library fusion protein #49.
                                                                                                                                                                                                           06-MAY-2004
                                                                                                                                                                                                                                                                                                            ADK15667 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 105; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-033956/03.
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20-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library fusion
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PEELLE B R.
BOGENBERGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.0%;
Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DAAAAEAAAKAAAEAAAKAAAEAA 27
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99US-00415765.
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                                                                                                                                                                                                                                                                                                            59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                 scaffold protein;
                                                                              sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 25
ADE10697
ID ADE106
XX ADE106
AC ADE10
XX Struc
XX Struc
XX Struc
XX Husic
KW Phenc
KW Cell
KW Unson
KW Lloss
KW Lloss
KW Lloss
KW Lloss
KW Unson
KW Scafi
XX Synth
XX Synth
XX US200
XX Synth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                     fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; prosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endogrinology; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
                                                                                                                                                                              drug toxicity; dr
scaffold protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                             Structurally biased random peptide library scaffold protein seqid 104.
                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE10697 standard; protein; 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-2002;
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08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAR-2003; 2003US-00393449
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                                                                                                       US2003143562-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ANDE/) ANDERSON D. (PEEL/) PEELLE B R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BOGE/)
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, 99US-00415765.
2002US-00177725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                      grug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%;
                                                                                                                                                                                                        resistance;
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Pred. No. 0
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20-JUN-2002; 2002US-00177725.

31-JUL-2003.

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RESULT 26
ADE10647
ID ADE10
XX
AC ADE10
XX
DT 29-JA
XX
                                                                                                                                                                                                                                                                                                                                                                                                         cc peptides conferring a change in specific phenotype such as cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more CC cells, and cellular density; changes in the expression of one or more CRNAS, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAS, protein, CC lipids, hormones, cytokines, or other molecules; ctanges (ci.e., the bioactive peptide), or one or more RNAS, protein, CC peptide identified by above mentioned method is used to generate more cc candidate peptides and to identify target molecules, i.e., the molecules candidate peptides and to identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic crelationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be cintroduced into any tumour cell (primary or cultured), and peptides cremening of bioactive peptides which restore the constitutive function of the broa-1 or broa-2 genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis coli gene (C eall-cell junctions, The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin cell-cell junctions, inflammation, bone biology applications, skin cell-cell junctions, industried applications, drug toxicities and drug resistance applications, mad altergic consistance applications, and biotechnology, inflammation, and altergic consistance applications, and altergic consistance applications, and biotechnology applications and thus increase the hit rate for targets that bind such cells bias and thus increase the hit rate for targets that bind such used in cells and cell with the libraries of a scaffold protein used in cells and cell interacted the libraries of hold the l
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening
                       29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-1998;
08-OCT-1999;
                                                                   ADE10647;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson D,
                                                                                                          ADE10647 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                   ХАЕААЕКААКҮААЕААЕКААКАХА 25
                                                                                                                                                                                                                         DAAAAEAAAKAAAEAAAKAAAEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 104; 110pp; English.
                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peelle BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               describes a library (I) of fusion nucleic acids, who cacid comprises a first nucleic acid (N1), encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00169015
99US-00415765
                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                    60.0%;
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                                                                                                            67
                                                                                                                                                                                                                                                                                                             Score 63; DB 7; Length 67; Pred. No. 0.37; Indels
                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                               Gaps
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tumour suppressor gene; breast cancer; adenomatous polyposis coll; APC; brosophila discs-large; DIg; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response.
                                                                                                                                                                                                                                     fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; cost cell division; decreased cell growth; brca-1; brca-2;
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Structurally biased random peptide library related protein seqid 54.

Synthetic

US2003143562-A1

20-JUN-2002; 2002US-00177725

08-OCT-1998; 08-OCT-1999; 98US-00169015. 99US-00415765.

(RIGE-) RIGEL PHARM INC

Anderson D, Peelle BR, Bogenberger JM;

WPI; 2003-829786/77.

Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening

Example 6; SEQ ID NO 54; 110pp; English

CC peptides conferring a change in specific phenotype such as cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more CC enls, and cellular density; changes in the expression of one or more CC lipids, hormones, lipids, hormones, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, CC lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, CC lipids, hormones, cytokines, or other molecules, i.e., the bioactive peptide identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined combined with other pharmacologic activators. Random libraries can be constituted into any tumour cell (primary or cultured), and peptides can be conscitutive peptides which restore the conscitutive function conference of the broa-1 or broa-2 genes, and other tumour suppressor genes conscitutive functions. The methods are useful in cardiovascular components of cell-cell junctions, cosmeceutical applications, and altergic resistance applications, immunoblology, inflammation, and altergic corresponse applications, and biotechnology applications. The peptide response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention. scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a (N2),

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RESULT 27
ADK15666
ID ADK15667
AC ADK15
XX ADK15
XX ADK15
XX AUCle
XX Husic
XX Mucle
XX Mucle
XX Green
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                                                                                        Query Match
Best Local S
Matches 16
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Best Local
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08-OCT-1999;
20-JUN-2002; 20
                                                                                                                                                                                                                                                      The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nuclearing sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence:
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                                                                                                                                                                                       Sequence 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-033956/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion nucleic acid library; fusion protein library; scaffold protein;
green fluorescent protein; GFP; alpha helical biasing sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK15666 standard; peptide; 67
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                                                                                          l Similarity
16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANDERSON D.
PEELLE B R.
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                                     XAEAAEKAAKYAAEAAEKAAKAXA
DAAAAEAAKAAAEAAAKAAAEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
                                                                                        60.0%;
nilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence; screening.
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99US-00415765.
2002US-00177725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              د،
ح
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bogenberger
                                                                                        ; Score 63; DB; Pred. No. 0.37
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                                                                                                                                       Length 67;
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RESULT 28 ADK15716 ID ADK15

ADK15716 standard; peptide;

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skin biology; cosmeceutical;

endocrinology;

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                                                                                                                                                                                                               RESULT 29
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
           fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; Drosophila discs-large; DIg; cardiovascular; neurobiology; bone biology;
                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helicibiasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a scaffold protein.
                                                                                                                                                                                                                                                                                                                                                               Sequence 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion nucleic acid library; fusion protein library; scaffold protein;
green fluorescent protein; GFP; alpha helical biasing sequence;
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                                                                                                      Structurally biased random peptide library scaffold protein seqid
                                                                                                                                  29-JAN-2004
                                                                                                                                                                                    ADE10696 standard; protein; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 104; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-033956/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson
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(BOGE/)
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20-JUN-2002;
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99US-00415765.
2002US-00177725.
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Pred. No.
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0.37;
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                                                                                                                                                                                                                                                                                                                                                                                                                      screening
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comorphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more CRNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, Clipids, hormones, cytokines, or other molecules; etc. The bicactive peptide identified by above mentioned method is used to generate more condidate peptides and to identify target molecules, i.e., the molecules cubic with which the bicactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic concluded into any tumour cell (primary or cultured), and peptides confirmed interded into any tumour cell (primary or cultured), and peptides cidentified which by themselves induce apoptosis, cell death, loss of cell civision or decreased cell growth. The method is also useful for correction of the broa-1 or broa-2 genes, and other tumour suppressor genes confirmed that breast cancer such as the adenomatous polyposis coli gene (APC) and the Drosophila discs-large gene (DIg), which are components of cell-cell-cell junctions. The methods are useful in cardiovascular
applications, infectious disease applications, drug toxicities and drug resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a scaffold protein used in peptide libraries ot hold the library peptide in a conformationally
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08-OCT-1999;
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99US-00415765
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XAEAAEKAAKYAAEAAEKAAKAXA 25 :| ||| ||| ||| ||| || :|

Query Match Best Local S Matches 16

l Similarity 16; Conserv

Conservative

Score 63; Pred. No. Pred. No. 0.4: 2; Mismatches

DB 7;

Length 75;

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Sequence

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                                                      CC scaffold protein sequence; and a second nucleic acid (N2), encoding a combinary peptide sequence comprising an alpha helical biasing sequence; CC where N1 is fused to N2. Disclosed is a method for screening bloactive peptides conferring a change in specific phenotype such as cell cells, and cellular density; changes in the expression of one or more CC cells, and cellular density; changes in the expression of one or more CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, clipids, hormones, cytokines, or other molecules; changes CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein, clipids, hormones, cytokines, or other molecules; changes CC inpids hormones, cytokines, or other molecules; cetc. The bioactive combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic crelationships of signal transduction pathways in question. The disclosed combined which by themselves induce apoptosis, cell death, loss of cell civision or decreased cell growth. The method is also useful for content in breast cancer such as the adenomatous polyposis coli gene components of cell-cell junctions. The methods are useful in cardiovascular coliportant in breast cancer such as the adenomatous polyposis coli gene cancer such as the adenomatous polyposis coli gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lalpha helical biasing sequence, respectively, useful in screening
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                                      applications, neurobiology applications,
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99US-00415765
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Best Local (
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                            The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a scaffold protein.
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08-OCT-1999;
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                                                                                                                                                     Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleating sequence; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion nucleic acid library; fusion protein library; scaffold protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-2004
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                                                                                                                                                                                                  scaffold
                                                                                                                                                                                                                                                 WPI; 2004-033956/03
                                                                                                                                                                                                                                                                            Anderson D,
                                                                                                                                                                                                                                                                                                                           (ANDE/)
                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library fusion
                                                                                                                                                                                                                                                                                                             (BOGE/)
                                                                                                                                                                                                                                                                                                           ANDERSON D. PEELLE B R. BOGENBERGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ХАЕАЛЕКЛАКУАЛЕЛЛЕКЛАКАХА 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Conservative
                                                                                                                                                                             of fusion polypeptides in which each polypeptides comprises
d protein and library peptide having alpha helical biasing
e, or scaffold protein, library peptide and nucleating sequence.
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99US-00415765.
2002US-00177725.
                                                                                                                                                                                                                                                                              Peelle
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                                                                                                                                                                                                                                                                            Bogenberger JM;
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; Pred. No. 0.42
2; Mismatches
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1.42;
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Best Local Similarity

60.0%;

Score Pred.

No.

DB 8; 0.42;

DB

Length

75;

ADE10695

ADE10695 standard;

protein;

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Query Match

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RESULT 33
ADE10695
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence; nucleating sequence; screening.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ANDE/)
(PEEL/)
(BOGE/)
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08-OCT-1999;
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PEELLE B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAAAAEAAAKAAAEAAKAAAEAA 27
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Pred. No. 0.42
2; Mismatches
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peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide (a) can be combined with other pharmacologic activators to study the epistatic relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be introduced into any timour cell (primary or cultured), and spetides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the broar-love peptides which restore the constitutive function and the broar-love peptides which restore the constitutive function of the broar-love peptides which restore the constitutive function and the broar-love peptides which as the adenomatous polyposis coli gene
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coli; APC; prosophila discs-large; DIG; cardiovascular; neurobiology; bone biology skin biology; cosmeceutical; endocrinology; infectious disease; drug cxicity; drug resistance; inflammation; allergic response;
                                                                      biology applications, cosmecentical applications, endocrinology applications, infectious disease applications, drug toxicities and drug resistance applications immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural place of the period of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (APC) and the Drosophila discs-large gene (DIg), which are components of cell-cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin hillow, and in the components of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive
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                      fusion nucleic acid comprises a first nucleic acid (NI), encoding a coaffold protein sequence; and a second nucleic acid (N2), encoding a clibrary peptide sequence comprising an alpha helical biasing sequence; where NI is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell comprising a period of the substrates or other cells, and cellular density; changes in the expression of one or more CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules; i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic
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Best Local
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08-OCT-1999;
20-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence;
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                                                                                                             Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                                                                                                                                                           WPI; 2004-033956/03
                                                                                                                                                                                                                                                                                                                                                                                        (ANDE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK15714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK15714 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APC) and the Drosophila discs-large gene (DIg), which are components of cell-cell junctions. The methods are useful in cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57
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                                                                                                                                                                                                                                                                                                                                                                                        ANDERSON D. PEELLE B R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rescent protein; GFP; sequence; screening.
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99US-00415765.
2002US-00177725.
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                                                                                                                                                                                                                                                                                                BR,
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Pred. No. 0.47
2; Mismatches
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The invention comprises a library of fusion nucleic acids, where each

Matches Best Query Match

Local

l Similarity 16; Conserv

Conservative

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Mismatches

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60.0%; 66.7%;

Score 63; I Pred. No. 0.

DB 8; . 47;

Length 83;

Sequence 83

B

102; 110pp; English.

Disclosure; SEQ ID NO

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RESULT 36
ADK15664
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Best Local
                                      The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein - GPP) and a library poptide sequence comprising an alpha helical biasing sequence, or a scatfold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a scaffold protein.
                                                                                                                                                                                                                                                                                                                                                       08-OCT-1998; 98US-00169015.
08-OCT-1999; 99US-00415765.
20-JUN-2002; 2002US-00177725.
                                                                                                                                                                              Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                                                                                                                                                          WPI; 2004-033956/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               green fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleating
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                                                                                                                                                     Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion nucleic acid library; fusion protein library; scaffold protein;
green fluorescent protein; GFP; alpha helical biasing sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK15664 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoded protein contains a scaffold protein (e.g. a green fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                               ANDERSON
PEELLE B
                                                                                                                                                     6; SEQ ID NO 52; 110pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence;
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Pred. No. 0.47
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AXAEAAEKAAKYAAEAAEKAAKAX 24

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RESULT 37
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                                                                                                                                                                            CC fusion nucleic acid comprises a first nucleic acid (N1), encoding a CC scaffold protein sequence; and a second nucleic acid (N2), encoding a CC library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell cc morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more CC in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; changes cin the equilibrium state (i.e., half-life) or one or more RNAs, protein, clipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more CC candidate peptides and to identify target molecules, i.e., the molecules combined with other pharmacologic activators to study the epistatic crelationships of signal transduction pathways in question. The disclosed controduced into any tumour cell (primary or cultured), and peptides controduced which by themselves induce apoptosis, cell death, loss of cell cidentified which by themselves induce apoptosis, cell death, loss of cell correction or decreased cell growth. The method is also useful for correction to study the epitides which restore the constitutive function constitutive function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; rumour sumpressor cans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide I
                                    screening of bioactive peptides which restore the constitutive find the brca-1 or brca-2 genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis col: (APC) and the Drosophila discs-large gene (DIg), which are componed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   second nucleic acids encoding scaffold protein and library peptide alpha helical biasing sequence, respectively, useful in screening
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08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structurally biased random peptide library related protein seqid 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE10642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a library (I) of fusion nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; SEQ ID NO 49; 110pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RIGE-) RIGEL PHARM INC
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99US-00415765.
discs-large gene (DIg), which are components of methods are useful in cardiovascular
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RESULT 38
ADE10692
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology applications, infectious disease applications, endocrinology resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIg; cardiovascular; neurobiology; bone biology skin biology; comecœutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular dansity; cancer; tumour; apoptosis; cell loss of cell division; decreased cell growth; brca-1; brca-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                       08-OCT-1998;
08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structurally biased random peptide library scaffold protein seqid 99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004
                                                                                                                                                                                                                                                                     Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003143562-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE10692 standard; protein;
                                                                                                                                                                                                                                                                                                      (RIGE-) RIGEL
                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2002; 2002US-00177725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           АХАЕААБКААКҮААБААБКААКАХ 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAKAAAEAAAKAAAEAAAKAAAAK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                     Peelle BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                      PHARM INC
                                                                                                                                                                                                                                                                                                                                     98US-00169015.
99US-00415765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%;
                                                                                                                                                                                                                                                                     Bogenberger JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63; DB
Pred. No. 0.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurobiology; bone biology;
infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening

scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive

conferring a change in specific

phenotype such as

The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (N1), encoding a

Disclosure;

SEQ ID

8

99;

110pp; English

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RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC cells, and cellular density; changes in the expression of one or more CC RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, CC lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more CC candidate peptides and to identify target molecules, i.e., the molecules candidate peptides and to identify target molecules, i.e., the molecules combined with other pharmacologic activators to study the epistatic crelationships of signal transduction pathways in question. The disclosed comethod is also useful in cancer applications. Random libraries can be introduced into any tumour cell (primary or cultured), and peptides contentified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for CC division or broa-2 genes, and other tumour suppressor genes CC important in breast cancer such as the adenomatous polyposis coli gene CC important in breast cancer such as the adenomatous polyposis coli gene CC applications, neurobiology applications, bone biology applications, skin CC applications, infectious disease applications, bone biology applications, skin CC applications, and biotechnology applications, and allergic cresistance applications, and biotechnology applications. The peptide CC library can easily be monitored, both for its presence within cells and CC elevated cellular concentration of structurally biased libraries generate CC elevated cellular concentration of peptides having a given structural CC bias and thus increase the hit rate for targets that bind such concentration acid sequence of a scaffold protein used in centracted bias and thus increase the hit rate for targets that bind such concentrations are periode in a conformationally cc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                                                   08-OCT-1998;
08-OCT-1999;
20-JUN-2002;
                                                                                                                                                                                                                                         18-MAR-2003;
                                                                                                                                                                                                                                                                                                  04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                          US2003224412-A1
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion nucleic acid library; fusion protein library; scaffold protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library fusion protein-related scaffold protein #43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK15711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK15711 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                morphology,
                               (ANDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fluorescent protein; GFP; alpha helical biasing sequence. ating sequence; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Н
) ANDERSON D.
) PEELLE B R.
) BOGENBERGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aakaaaeaaakaaaeaakaaak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                         2003US-00393449.
                                                                                                                      2002US-00177725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                               98US-00169015.
99US-00415765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63; DB
Pred. No. 0.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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0.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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و
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or other
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밁 Ś

encoded protein biasing

Example

6; SEQ ID NO 49; 110pp; English

The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha hel biasing sequence, or a scaffold protein, a library peptide and a

helical

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RESULT 40
ADK15661
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein - GPP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a mucleating sequence. The library of the invention is useful for screening bloactive peptides conferring a particular phenotype. The present amino acid sequence represents a scaffold protein.
                                                                                                                                                                                                                                                                                                                                   green fluorescent protein; nucleating sequence; screer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                                 WPI; 2004-033956/03.
                                                                                                                                                                     (ANDE/)
                                                                                                                                                                                                    08-OCT-1999;
20-JUN-2002;
                                                                                                                                                                                                                          08-OCT-1998;
                                                                                                                                                                                                                                                                    04-DEC-2003
                                                                                                                                                                                                                                                                                          US2003224412-A1
                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                             fusion nucleic acid library; fusion protein library; scaffold protein;
green fluorescent protein; GFP; alpha helical blasing sequence;
                                                                                                                                                                                                                                                                                                                                                                               Nucleating
                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADK15661 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson D,
                                                                                  scaffold protein
                                                                                                                                    Anderson D,
                                                                                                                                                                                                                                              18-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                     ANDERSON
PEELLE B
                                                                     of fusion polypeptides in which each polypeptides comprises
d protein and library peptide having alpha helical biasing
e, or scaffold protein, library peptide and nucleating seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                           BOGENBERGER J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AXAEAAEKAAKYAAEAAEKAAKAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAKAAAEAAAKAAAEAAAKAAAAK 86
                                                                                                                                                                                                                                                                                                                                                                               sequence-containing library fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 99; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                   98US-00169015.
99US-00415765.
2002US-00177725.
                                                                                                                                     Peelle
                                                                                                                                                                                                                                               2003US-00393449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peelle
                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.0%;
                                                                                                                                    BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BR,
                                                                                                                                                                                                                                                                                                                                    screening.
                                                                                                                                    Bogenberger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bogenberger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ).5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                       sequence
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Best Local
          fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where N1 is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bloactive peptide identified by above mentioned method is used to generate more
                                                                                                                                                                                                                                                                                                                       Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lalpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; loss of cell division; decreased cell growth; brca-1; brca-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; Drosophila discs-large; DIg; cardiovascular; neurobiology; bone biology; skin biology; cosmecceutical; endocrinology; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 88
                                                                                                                                                                                                                        The invention describes a library (I) of fusion nucleic acids, where each
                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-2002; 2002US-00177725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scaffold protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Structurally biased random peptide library scaffold protein segid 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE10694 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxicity; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAKAAAEAAAKAAAEAAAKAAAAK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                      SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00169015.
99US-00415765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resistance; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%;
                                                                                                                                                                                                                                                                  101; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bogenberger JM
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Pred. No. 0.
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0.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be introduced into any tumour cell (primary or cultured), and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the broa-1 or broa-2 genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis coll gene (APC) and the Drosophila discs-large gene (DIg), which are components of cell-cell junctions. The methods are useful in cardiovascular
                                                                                                                                                                                                                                                       response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a scaffold protein used i peptide libraries ot hold the library peptide in a conformationally
                                                                                                                                                                                          Sequence 91
                                                                                                                                                                                                                                                                                                                                                                                                                                    applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology applications, infectious disease applications, disease applications, disease applications, disease applications, and allergic resistance applications, immunobiology, inflammation, and allergic
                                                                                              16;
                                                                                                                       Similarity
                                           AXAEAAEKAAKYAAEAAEKAAKAX 24
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K
                                                                                           Conservative
                                                                                                                  60.0%;
66.7%;
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                                                                                                                     Score 63; DB 7
Pred. No. 0.52;
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tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; prosophila disce-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response. fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell loss of cell division; decreased cell growth; brca-1; brca-2; ADE10644 standard; protein; 91 Structurally biased random peptide library related protein seqid 29-JAN-2004 (first entry)

cell death;

51

US2003143562-A1

08-OCT-1998; 08-OCT-1999; 20-JUN-2002; 2002US-00177725. 98US-00169015 99US-00415765

Anderson D, (RIGE-) RIGEL Peelle BR, PHARM INC Bogenberger JM;

WPI; 2003-829786/77.

Novel library of fusion nucleic acids each of which has fused first and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, ilpids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be introduced into any tumour cell (primary or cultured), and peptides indentified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the brca-1 or brca-2 genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis coli gene
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology applications, infectious disease applications, and virus toxicities and drug resistance applications, immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such fused nucleic acid and random peptide libraries of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusion nucleic acid comprises a first nucleic acid (N1), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where NI is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more cells, and cellular density; changes in the expression of one or more cells.
                                       US2003224412-A1
                                                                                                                                                 fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence;
                                                                                                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                ADK15663 standard; peptide; 91 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APC) and the Drosophila discs-large gene (DIg), which are components of cell-cell junctions. The methods are useful in cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention
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                                                                                                                                nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAKAAAEAAAKAAAEAAAKAAAK 88
                                                                                                                                   sequence;
                                                                                                                                                                                                                 sequence-containing
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                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%;
66.7%;
                                                                                                                                screening.
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Pred. No.
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04-DEC-2003

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                                                                              08-OCT-1998;
08-OCT-1999;
20-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ANDE/)
(PEEL/)
(BOGE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
           Anderson D,
                                                                                                                                                 04-DEC-2003
                                                                                                                                                                       US2003224412-A1
                                                                                                                                                                                                                 nucleating
                                                                                                                                                                                                                             fusion nucleic acid library; fusion protein library; scaffold protein;
green fluorescent protein; GFP; alpha helical biasing sequence;
                                                                                                                                                                                                                                                              Library fusion protein-related scaffold protein #45
                                                                                                                                                                                                                                                                                       06-MAY-2004
                                                                                                                                                                                                                                                                                                                                  ADK15713 standard; peptide; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
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08-OCT-1999;
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                                              (ANDE/)
                                                                                                                          18-MAR-2003; 2003US-00393449
                                    (BOGE/)
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PEELLE B
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                                    BOGENBERGER J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOGENBERGER J M.
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99US-00415765.
2002US-00177725.
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             Peelle BR,
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99US-00415765.
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             Bogenberger
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Pred. No. 0.
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WPI; 2004-033956/03

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XX 29-JA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell alhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response;
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                                                                                                                                                                                  Novel library of fusion nucleic acids each of which has fused first second nucleic acids encoding scaffold protein and library peptide lalpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                                                                                                                          WPI; 2003-829786/77.
                                                                                                                                                                                                                                                                                                                                                                                      Anderson D,
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08-OCT-1999;
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99US-00415765.
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Pred. No. 0.
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CC candidate peptides and to identify target molecules. i.e., the molecules (CC with which the bioactive peptide interacts. The peptide(s) can be CC combined with other pharmacologic activators to study the epistatic CC relationships of signal transduction pathways in question. The disclosed CC introduced into any tumour cell (primary or cultured), and peptides can be CC introduced into any tumour cell (primary or cultured), and peptides cC identified which by themselves induce apoptosis, cell death, loss of cell CC division or decreased cell growth. The method is also useful for CC screening of bioactive peptides which restore the constitutive function of the brca-1 or brca-2 genes, and other tumour suppressor genes (APC) and the Drosophila discs-large gene (DIg), which are components of cell-cell junctions. The methods are useful in cardiovascular cc applications, neurobiology applications, bone biology applications, skin CC biology applications, infectious disease applications, drug toxicities and drug resistance applications, immunobiology, inflammation, and allergic cresistance applications, and biotechnology applications. The peptide CC response applications, and biotechnology applications. The peptide creased cellular concentration of structurally biased libraries generate concentration of structurally biased libraries generate concentration acid sequence of a scaffold protein used in peptide libraries of hold the library peptide in a conformationally creational conformationally creations. The scaffold protein used in peptide libraries of hold the library peptide in a conformationally creational conformationally creations.
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Query Match Best Local 9 Matches Similarity Conservative 60.0%; Score 63; DB Pred. No. 0.61 2; Mismatches 2 0.61; 7; 9 Length 104; Indels 0 Gaps

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Search completed: July 11, Job time: 163 secs 2005, 09:43:30

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fusion nucleic acid

describes a library (I) of fusion nucleic acids, where c acid comprises a first nucleic acid (N1), encoding a

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Result
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Sequence 15, Appl	Sequence 3, Appli	Sequence 12, Appl	Sequence 11, Appl	Sequence 10, Appl	Sequence 14, Appl	Sequence 13, Appl	Sequence 11, Appl	Sequence 10, Appl	•	Sequence 11, Appl	Sequence 10, Appl	Sequence 1, Appli	Sequence 12, Appl	Sequence 13678, A	Sequence 2, Appli	Sequence 5, Appli	Sequence 5, Appli

ALIGNMENTS

## US-09-902-540-14824 US-09-902-540-14824 PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10 NUMBER OF SEQ ID NOS: 16825 SEQ ID NO 14824 LENGTH: 69 Sequence 14824, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION: Matches Best Local Similarity Query Match APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C. APPLICANT: Wiegand, Roger C. APPLICANT: Wiegand, Roger C. TITLE OF INVENTION: Myxococcus xanthus Genome FILE REFERENCE: 38-10(1584)B CURRENT APPLICATION NUMBER: US/09/902,540 CURRENT FILING DATE: 2001-07-10 LENGTH: 69 TYPE: PRT ORGANISM: Myxococcus xanthus 12 16; 1 AXAEAAEKAAKYAAEAAEKAAKAXA 25 |: ||| ||| |||| :||:|:| AAKRAAEAAAKRAAEAARRAAEAAA 36 Conservative 64.8**%**; 4; Mismatches Score 68; DB 4; Pred. No. 0.018; Sequences Length 69; 0 Gaps

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US-09-405-743A-3

Sequence 3, Application US/09405743A Patent No. 6514938

SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 56
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE

SYNTHETIC

GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEC ID NOS: 7

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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR THERAPEUTIC USE FILE REFERENCES: 2609/68007-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A · CURRENT FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR PILING DATE: 1998-09-25 PRIOR APPLICATION NUMBER: PCT/US99/22402 PRIOR FILING DATE: 1998-09-24 PRIOR FILING DATE: 1999-09-24 NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin version 3.1
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LENGTH: 86
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Patent No. 6514938
GENERAL INFORMATION:
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US-08-303-025-16
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR PEPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09816989A
Patent No. 6800287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5614494
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
               FILING DATE: 08-SEPT-1994
CIASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                               MEDIUM TYPE: Floppy diskette 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: Wordperfect 6.1; ASCII
CURRENT APPLICATION NUMBER: US/08/303,025
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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STREET:
OTTY: Detroit
Michi
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    150 West Jefferson, Suite
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                                                                               PCT/US92/06829
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SOFTWARE: ASCII (LUC), ...

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAX-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: N/A
FILING DATE: N/A
FILING DATE: N/A
ATTORNEY/ACENT INFORMATION:
NAME: ROHM, Benita J.
REGISTRATION NUMBER: 7WK-06054
REFERENCE/DOCKET NUMBER: 7WK-06054
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 11FORMATION:
TELECOMMUNICATION 11FORMATION:
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AUTHORS: N/A
TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-303-025-16
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3equence 4, App. ...
3equence 4, App. ....
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
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ORIGINAL SOURCE:
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Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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Detroit
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                                                                                                                                                                                                                                                                                                                                                                                                           United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wakefield, Thomas W.
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                                                                      7WK-060548-00233
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Pred. No. 0.067;
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SEQ ID NO 13565
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APPLICANT: Gary Betton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                     SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/09340736E Patent No. 6489446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local (
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                      PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
                                                                                                                                            TITLE OF INVENTION: SÉLF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN TITLE OF INVENTION: AND OTHER FIROUS PROTEINS FILE REFERENCE: 041082/0110 CURRENT APPLICATION NUMBER: US/09/340,736E CURRENT FILING DATE: 1997-06-29 PRIOR APPLICATION NUMBER: 08/911,364 PRIOR FILING DATE: 1997-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 2709.2004001
CURRENT APPLICATION UNMERS: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                         APPLICANT: ROTHSTEIN, ASER
APPLICANT: KEELEY, FRED
APPLICANT: ROTHSTEIN, STEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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ORGANISM: Artificial Sequence
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ORIGINAL SOURCE:
                                    ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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66.7%;
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 Mismatches

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Pred. No. 1.3;
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Pred. No. 0.
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0.067;
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: MFU-4 polypeptide US-09-340-736E-10
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US-09-340-736E-9
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-662-9
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                                                                                                                                         PRIOR APPLICATION NUMBER: 08/911,364
PRIOR FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09340736E Patent No. 6489446 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
TITLE OF INVENTION: OTHER PIBROUS PROTEINS
FILE REFERENCE: 041082/0112
FILE REFERENCE: 041082/0112
CURRENT APPLICATION NUMBER: US/09/964,662
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: 09/340,736
PRIOR PILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS FILE REFERENCE: 041082/0110 CURRENT APPLICATION NUMBER: US/09/340,736E CURRENT FILLING DATE: 1999-06-29
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROTHSTEIN, ASER APPLICANT: KEELEY, FRED APPLICANT: ROTHSTEIN, STE
                                                                                                   LENGTH: 118
TYPE: PRT
                                                                           ORGANISM: Artificial Sequence
                                                          FEATURE:
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ROTHSTEIN, STEVEN
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Pred. No. 0.
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Query Match

57.6%;

Score

60.5;

DB 4;

Length 118;

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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-964-662-10
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US-09-964-662-10
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SEQ ID NO 11
LENGTH: 199
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                                                           Query Match 57.6%;
Best Local Similarity 58.6%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6489446
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APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
TITLE OF INVENTION: OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0112
CURRENT APPLICATION NUMBER: US/09/964,662
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: 09/340,736
PRIOR APPLICATION NUMBER: 09/340,736
PRIOR FILING DATE: 1999-06-29
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR FILING DATE: 1997-08-07
PRIOR APPLICATION NUMBER: 60/023,552
PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS FILE REFERENCE: 041082/0110
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                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: MFU-5 polypeptide
                                                                                                                                                                                                                                   TYPE: PRT
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AXAEAAEKAAKY-----AAEAAEKAAKAX 24
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ROTHSTEIN, ST
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                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: MFU-1 polypeptide US-09-340-736E-2
                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS FILE REFERENCE: 041082/101.
CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
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APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
TITLE OF INVENTION: OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0112
CURRENT APPLICATION NUMBER: US/09/964,662
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: 09/340,736
PRIOR APPLICATION NUMBER: 09/340,736
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEC IN NO. 59-06-29
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                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/023,552
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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nes 17; Conserv
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                                         1 AXAEAAEKAAKY-----AAEAAEKAAKAX 24
AQAAAAAKAAKYGVGTPAAAAAKAAAKAA 66
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ROTHSTEIN, STEVEN
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                                                                                          Conservative
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                                                                                                          57.6%;
                                                                                   Score 60.5; DB Pred. No. 0.59; 3; Mismatches
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US-08-911-364-2
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TELEFAX: (202) TELEFAX: (202) TELEFAX: (202) TELEFAX: 2: SEQUENCE CHARACTERISTICS: TENGTH: 201 amino acids
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LENGTH: 200
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APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
TITLE OF INVENTION: OTHER FIBROUS PROTEINS
FILE REFERENCE: 041082/0112
CURRENT APPLICATION NUMBER: US/09/964,662
CURRENT FILING DATE: 2003-05-08
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PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 11
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                                                                                                                   NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 07-AUG-199
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                               APPLICATION NUMBER: US 6
FILING DATE: 07-AUG-1996
ATTORNEY PAGENT INFORMATION:
                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 20007-5109
                                                                                                  TELEPHONE:
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                                                                                                       (202)
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58.6%;
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-403-8
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Matches 17; Conserv
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CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
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APPLICANT: HAENDLER,
APPLICANT: KRAETZSCH
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: REGIDOR, PEDRO
APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRICSIS
FILE REFERENCE: SCH-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  APPLICANT: ROTHSTEIN, Steven J.
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                         COUNTRY: U.S.A. ZIP: 20007-5109
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APPLICATION NUMBER: US/08/911,364 FILING DATE: 07-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08911364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRAETZSCHMAR, JOERN
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58.6%;
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 Mismatches

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Pred. No. 0.6;
                                                     Version #1.30
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-736E-1
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                                                                                                                                                            US-09-964-662-1
                                                                                                                                                                               RESULT 21
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US-09-340-736E-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: ROTHSTEIN, ASER
APPLICANT: KEELEY, FRED
APPLICANT: KEELEY, FRED
APPLICANT: ROTHSTEIN, STEVEN
APPLICANT: ROTHSTEIN, STEVEN
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN
TITLE OF INVENTION: AND OTHER FIBROUS PROTEINS
                                                                                         Sequence 1, Application US/09964662
Patent No. 6765086
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                              Query Match
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                  APPLICANT: PROTEIN SPECIALTIES LTD.
APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN ELASTIN AND
TITLE OF INVENTION: OTHER FIBROUS PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1996-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/340,736E
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 08/911,364
PRIOR FILING DATE: 1997-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO:
FILE REFERENCE: 041082/0112
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APPLICATION NUMBER: US 60/023,552
FILING DATE: 07-AUG-1996
ATTORNEY/ACENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 731 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                         415 AQAAAAAKAAKYGVGTPAAAAAKAAAKAA 443
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58.6%;
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58.6%;
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Pred. No. 2.
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RESULT 22
US-08-464-700-2
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; SEQ ID NO 1
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo Bapiens
US-09-964-662-1
                                                                         US-08-464-700-2
Query Match
Best Local Similarity 58.6
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08464700 Patent No. 6232458
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Best Local :
                                                                                                                                                   TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PL9661

FILING DATE: 28-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU93/00

FILING DATE: 16-DEC-1993

ATTORNEY/AGENT INFORMATION:
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CURRENT FILING DATE: 2003-05-08
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                                                                                      TYPE: amino acids
TOPOLOGY: line

OLECHT
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/OFFILING DATE: 7-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WEISS, ANTHONY S
APPLICANT: MARTIN, STEPHEN L
                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Spring House
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: AU PL6520 FILING DATE: 22-DEC-1992
                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                           NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
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Similarity 58.6%;
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Spring House Corporate Cntr, PO Box 457
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         3; Mismatches
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Pred. No. 2.5;
3; Mismatches 4;
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SOFTWARE: Par
; SEQ ID NO 2
"SNIGTH: 45
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CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: PCT/DE00/00061
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: DE 199 00 513.3
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: DE 199 33 939.2
PRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 15
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APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09405743A Patent No. 6514938
                                      Matches
                                                                         Query Match
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Patent No. 6521456
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EQ ID NO 7
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TITLE OF INVENTION: USE OF CELLULAR TRANSPORT SYSTEMS
TITLE OF INVENTION: THROUGH THE NUCLEAR ENVELOPE
FILE REFERENCE: 30430.1USWO
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
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APPLICANT: Christine, R
                                                                                                                             ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
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                                    / Match 56.2%;
Local Similarity 58.3%;
les 14; Conservative
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                                    Score 59; DB 4
Pred. No. 0.18;
3; Mismatches
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SEQ ID NO 7
LENGTH: 109
                                                       Sequence 7, Application US/09816989A Patent No. 6800287 GENERAL INFORMATION:
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Best Local &
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Best Local
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 TITLE
                 APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
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OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
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AEAKKAEAAKAYKAEAAKAAAKEAA 106
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58.3%;
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FITTLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN OF SEQ ID NOS: 7
SOFTWARE: PATENTIN OF SEQ ID NOS: 7
SOFTWARE: PATENTIN OF SEQ ID NOS: 7
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LENGTH: 77
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Best Local Similarity
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKITITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-24
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                        APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Local Similarity 56.0%;
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Pred. No. 0.47;
4; Mismatches
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Pred. No. 0.44;
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Query Match Best Local

54.8%;

Score 57.5; Pred. No. 2

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Length 325;

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RESULT 31
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US-09-344-529-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Myoxocephalus scorpius US-09-344-529-2
US-09-902-540-13678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-06-26
EARLIER APPLICATION NUMBER: US 60/095,713
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 92
                                                  PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 13678
LENGTH: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09344529 Patent No. 6429293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                Sequence 13678, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                        APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/344,529
CURRENT FILING DATE: 1999-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hew, Choy L.
APPLICANT: HSC Research and Development Limited Partnership
TITLE OF INVENTION: Sculpin-Type Antifreeze Polypeptides and Nucleic Acids
FILE REFERENCE: 016252-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENERAL INFORMATION:
                                                                                                                                                                                                                                                                     APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                    ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/090,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AYAKKAEKAAKKAEAKAYKAAEAKKKAKAEA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 АХАЕААЕКААК-----УЛАЕЛАЕКААКАХА 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAKAAEAAAMAAANAAEAAATKAA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.2%;
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51.6%;
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Pred. No. 0.53;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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Pred. No. 0.44;
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US-08-303-025-12
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                                                                                                                 DOCUMENT NUMBER: PCT/US92/08069; FILING DATE: 14-AUG-1993
US-08-303-025-12
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                                                                                Query Match
                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION APPLICANT: Wakef
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSITICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/U:
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08,
FILING DATE: 12-NOV-1993
                                                                                                                                                                                                                                                                                                                            TELEFAX: 313-496-8454 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy diskette 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6.1; ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Rohm, Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                         PUBLICATION INFORMATION
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                          AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 150 West
CITY: Detroit
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 08-SEI
                                                      Local Similarity 56.
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Rohm, Benita J. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 48226-4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: N/
                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 313-496-7622
                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAKRAAEAAKKAAEAAAKKTAEAAA 45
PAKKAKKAAKKAKKAAKKAA 23
                          XAEAAEKAAKYAAEAAEKAAKAX 24
                                                                                                                                                              N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B: Benita J, Rohm, Esq.
150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                             28 amino acids
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                                                                                                                                                                                                                                                                                                                                             313-496-8454
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                                                                                                                                                                                                                                                    N/A
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                                                                                                                                                                                                                                     peptide
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                                                                     56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 James C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOVEL PEPTIDES FOR HEPARIN AND LOW MOLECULAR WEIGHT HEPARIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 08/152,488
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                                                                       Score 57; 1
Pred. No. 0
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                                                         Mismatches
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                                                                                     DB 1;
                                                                                   Length 28;
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RESULT 34
US-08-152-488-10
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AUTHORS: N/A
TITLE: N/A
US-08-436-703B-1
                                                                                                        Sequence 10, Application US/08152488 Patent No. 5534619
                                                                                                                                                                                                                                                                                          Query Match 54.3
Best Local Similarity 56.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08436703B Patent No. 5919761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
APPLICANT: Wakefield, Thomas w.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR
TITLE OF INVENTION: HEDARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
                          GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Wakefi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/
FILING DATE: 08-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UDMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordberfect 6;
SOFTWARE: ASCII (DOS)Text
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-965-1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: N/A MOLECULE TYPE: I ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Michigan COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6601 Woodw
STREET: Suite 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: N/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
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                                                                                                                                                                                                                     PAKKAKKAAKKAKKAAKKAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313-965-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N/A
                                                                                                                                                                                                                                                                                                             54.3%;
James C.
NOVEL PEPTIDES FOR HEPARIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/436,703B
                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                             Score 57; DB 2
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7WK-060548-00233
                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                          Length 28
                                                                                                                                                                                                                                                                                            Indels
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US-08-152-488-10
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                                                                                                                                                                                                                                                                                                                              RESULT 35
                                                                                                           Patent No. 5534619

GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                      Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: RM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOrdPerfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: LOW TITLE OF INVENTION: ANT NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: SINGLE Cranford
                               STREET: 512 Spi
CITY: Cranford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 54.3%; Local Similarity 56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Rohm, Benita : REGISTRATION NUMBER:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 29 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                         2 XAEAAEKAAKYAAEAAEKAAKAX 24
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                   New Jersey
                                                                                                                                                                                                                                                                                        Application US/08152488
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                                                   512 Springfield Avenue
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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READABLE FORM:

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; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-11
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATB: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/US
FILING DATE: 14-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                         tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                           SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                         APPLICANT: Andrews, Philip C
APPLICANT: Stanley, James C.
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: RM TELECOMMUNICATION INFORMATION: TELEPHONE: 908-276-3344
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                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Rohm, Benita J.
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE: N/A
                                                                                                                                                         CITY: Cranford
STATE: New Jersey
                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                           TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
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                                                                                                                            COUNTRY: United ZIP: 07016-1811
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                                                                                                                                                                                                                                                                                                                                                                                        Application US/08152488
                                                                                                                                                                                         512 Springfield Avenue
                                                                                                                                          United States of America
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                                                                                                                                                                                                        Benita J, Rohm, Esq
                                                                                                                                                                                                                         ADDRESS:
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2-NOV-1993
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                                                                                                                                                                                                                                                                       NOVEL PEPTIDES FOR HEPARIN AND LOW MOLECULAR WEIGHT HEPARIN
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           US/08/152,488
                                             6; ASCII (DOS) Text
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; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-12
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
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ORIGINAL SOURCE:
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                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                               APPLICATION NUMBER:
FILING DATE: 14-AUG-
APPLICATION NUMBER:
FILING DATE: 12-NOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS v.6.22 SOFTWARE: WordPerfect 6.1; ASCII
                                                                                                                                              APPLICATION NUMBER: FILING DATE: 08-SE
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                                                                                                                                                                                                                                                                                                             STATE:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER: 7WH-060548-00231
                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: N/
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150 West Jefferson,
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                                                 14-AUG-1992

NUMBER: US 08/152,488

12-NOV-1993
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                                                                                                PCT/US92/06829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomas W.
                                                                                                                                                            US/08/303,025
                                                                                                                                                                                                                                                                                                                                            Rohm, Esq.
ferson, Suite 2500
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                                                                                                                                                                                               (DOS) Text
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0.2;
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; FILING DATE: 14-AUG-1993
US-08-303-025-10
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Best Local Similarity
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Patent No. 561449
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                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                     APPLICATION NUMBER: US
FILING DATE: 08-SEPT-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PO
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5"
COMPUTER: IEM PC compatible
OPERATING SYSTEM: MS-DOS v.6.22
                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
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                                              SEQUENCE CHARACTERISTICS:
                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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PUBLICATION INFORMATION:
AUTHORS: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                         FILING DATE: 14-AU APPLICATION NUMBER: FILING DATE: 12-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 150 We
CITY: Detroit
TYPE: amino acid
STRANDEDNESS: N/
                                                                                            TELEPHONE:
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                               ENGTH:
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: United States of America
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150 West Jefferson, Suite 2500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andrews, Philip
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                                                                                             313-496-7622
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                                                                                                                                                                                         US 08/152,488
                                                                                                                                                                                                                         PCT/US92/06829
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                                                                                                                                                                                                                                                                                                                   6.1; ASCII (DOS) Text
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                                                                                                                            7WH-060548-00231
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; TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-11
; PTLING DATE: 14-AUG-1993
US-08-303-025-13
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US-08-303-025-13
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TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WORDERFECT 6.1; ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US92/0682
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 48226-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: N/A
PUBLICATION INFORMATION:
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                                                                                             ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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mes 13; Conserv
                                                                                                                                                                                                                                                                                                             NAME: Rohm, Benita J. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                  TITLE:
                                                                             AUTHORS:
                                                                                                                                                             FOPOLOGY:
                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                            ENGTH:
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                                                                N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michigan
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150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
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NOVEL PEPTIDES FOR HEPARIN AN LOW MOLECULAR WEIGHT HEPARIN ANTICOAGULATION REVERSAL
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Pred. No.
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FILING DATE: 14-AUG-1993
US-08-303-025-14
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Best Local
                                                                 Query Match
Best Local Similarity
                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14,
                                                                                                                                                                                                                                                                                                   TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: /Floppy
                                                                                                                                                                         PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                 TITLE: N/A
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APPLICATION NUMBER:
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                                                                                                                                                            AUTHORS:
                                                                                                                                                                                        ORGANISM:
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150 West Jefferson, Suite 2500
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VENTION: NOVEL PEPTIDES FOR HEPARIN AND
VENTION: LOW MOLECULAR WEIGHT HEPARIN
VENTION: ANTICOAGULATION REVERSAL
                                                                                                                                                                                                                                                                                                                313-496-8454
                                                      Conservative
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IBM PC compatible
SYSTEM: MS-DOS v.6.22
                                                                                                                                                                                                                 peptide
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UMBER: US_08/152,488
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                                                   Score 57; DB Pred. No. 0.2; 6; Mismatches
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0.2;
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FILING DATE: 14-AUG-1993
US-08-677-304-10
RESULT 42
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US-08-677-304-10
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Patent No. 5721212
                                                                                                                Matches
                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                               PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                 ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS) Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of ZIP: 07016-1811
                                                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                             2 ХАБААБКААКУААБААБКААКАХ 24
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512 Springfield Avenue
                                                                                                                                                                                                                                                                                                                                                                                               29 amino acids
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Andrews, Philip
                                                                                                                Conservative
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                                                                                                                              56.5%;
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                                                                                                                              Score 57; DB 1;
Pred. No. 0.2;
                                                                                                                Mismatches
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                                                                                                                Indels
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US-08-677-304-11

Patent No. 5721212
Patent No. 5721212
Patent INFORMATION:

Application

US/08677304

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RESULT 43
US-08-677-304-12
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-677-304-11
                                                                                                                                                                       Sequence 12, Application US/08677304 Patent No. 5721212
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELEPHONE: 908-276-3344
TELEPHONE: 908-276-5543
                                                                                                         GENERAL INFORMATION:
APPLICANT: Wakefi
APPLICANT: Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                          TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPAR TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARTITLE OF INVENTION: ANTICOAGULATION REVERSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPOLOGY: No. 5721212 Relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                  APPLICANT: Stanley, James C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE
                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New Jersey
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United ZIP: 07016-1811
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                                                                                                                                                                                                                                                                                                                                                                                         Local
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VENTION: NOVEL PEPTIDES FOR HEPARIN AND VENTION: LOW MOLECULAR WEIGHT HEPARIN
                                                                                                           Wakefield, Thomas W. Andrews, Philip C.
ADDRESS:
                                                    NOVEL PEPTIDES FOR HEPARIN AND LOW MOLECULAR WEIGHT HEPARIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTICOAGULATION REVERSAL
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                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       Score 57; DB Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                              Sequence 3, Application US/08436703B Patent No. 5919761
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/152,488
FILLING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGREYT INFORMATION:
NAME: Rohm, Benita J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOrdPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 6601 Woodward Avenue
                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                    NUMBER OF SEQUENCES:
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                         STREET: 6601 Woodwa
STREET: Suite 1525
CITY: Detroit
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nes 13; Conserv
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TYPE: amino acid
STRANDEDNESS: No. 5721
TOPOLOGY: No. 5721212 i
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CITY: Cranford
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America ZIP: 07016-1811
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                  Michigan
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United States of America
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5721212 Relevant
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                                                                                                                                        ANTICOAGULATION REVERSAL
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Pred. No. 0.2;
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US-08-436-703B-15
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; TITLE: N/A
US-08-436-703B-3
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Best Local Similarity 56.5
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY_AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-965-1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 313-965-1951
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              APPLICANT: Stanley, James C.
TITLE OF INVENTION: HEPARIN AND LOW MOI
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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OPERATING SYSTEM:
SOFTWARE: WordPer
                                                                                                                                                                                         STREET: Suite
CITY: Detroit
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TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                                                                          Michigan
                                                                                                                                                                                                           Suite 1525
                                                                                                                                                                                                                            6601 Woodward Avenue
                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                        Andrews, Philip C.
                                                                                                                                                                                                                                                                                                                                                                                                          Wakefield, Thomas W.
                               WordPerfect 6;
ASCII (DOS) Text
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NUMBER: US/08/436,703B
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                ON DATA:
                                                                                                                                                                                                                                                                                                HEPARIN AND LOW MOLECULAR WEIGHT HEPARIN ANTICOAGULATION REVERSAL
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                                           Best Local Similarity 56.5%;
Matches 13; Conservative
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                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                          ORGANISM: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Rohm, Benita J.
                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                     NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 0
CLASSIFICATION:
                                                                                                                                AUTHORS: N
TITLE: N/A
                                                                                                                                                                                                                                              ENGTH: 29 amino
                                                                                                                                                                                                                                                                                                                        TELEPHONE: 313-965-1976
                                                                                                                                                                                                                   TOPOLOGY: N/A
                                                                                                                                                                                                                            RANDEDNESS:
5 AAKKAKKAAKKAAKKAKKAA 27
                           2 XAEAAEKAAKYAAEAAEKAAKAX 24
                                                                                                                                                                                                                                                             29 amino acids
                                                                                                                                                                                                     peptide
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                                                         6; Mismatches
                                                                       Score 57; I
                                                                                    DB 2;
                                                         4; Indels
                                                                                   Length 29;
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Search completed: July 11, 2005, 09:47:56
Job time: 43 secs

Gaps

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Maximum DB seq length: 200000000
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l: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB_pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB_pep:*
/cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB_pep:*
/cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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gn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US099_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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gn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
gn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
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gn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-10-177-725-42 US-10-177-725-92 US-10-393-449-92 US-10-393-449-92 US-10-437-963-152005 US-10-282-122A-55748 US-10-667-004-21 US-10-667-004-24 US-10-177-725-49 US-10-177-725-89	ID
Sequence 42, Appl Sequence 92, Appl Sequence 42, Appl Sequence 92, Appl Sequence 152005, Sequence 55748, A Sequence 21, Appl Sequence 24, Appl Sequence 39, Appl Sequence 40, Appl Sequence 89, Appl	Description

14 64 61.0 104 15 US-10-393-449-40 Sequence 40, 163.6 61.0 104 15 US-10-393-449-89 Sequence 90, 177 63.5 60.5 104 14 US-10-177-725-41 Sequence 91, 18 63.5 60.5 104 14 US-10-177-725-91 Sequence 91, 19 63.5 60.5 104 15 US-10-393-449-91 Sequence 91, 20 63.5 60.5 104 15 US-10-393-449-91 Sequence 91, 21 63 60.0 59 14 US-10-177-725-55 Sequence 55, 22 63 60.0 59 15 US-10-393-449-10 Sequence 55, 23 63 60.0 59 15 US-10-393-449-10 Sequence 105, 25 63 60.0 59 15 US-10-393-449-55 Sequence 56, 26 63 60.0 67 14 US-10-177-725-54 Sequence 104, 26 63 60.0 67 14 US-10-177-725-54 Sequence 57, 26 63 60.0 67 15 US-10-393-449-54 Sequence 104, 27 63 60.0 67 15 US-10-393-449-54 Sequence 104, 27 63 60.0 75 14 US-10-177-725-53 Sequence 104, 27 63 60.0 75 14 US-10-177-725-53 Sequence 104, 27 63 60.0 83 14 US-10-177-725-53 Sequence 104, 27 63 60.0 83 15 US-10-393-449-103 Sequence 103, 31 63 60.0 83 14 US-10-177-725-10 Sequence 103, 31 63 60.0 83 14 US-10-177-725-10 Sequence 57, 31 63 60.0 83 15 US-10-393-449-10 Sequence 102, 31 63 60.0 83 15 US-10-393-449-10 Sequence 103, 32 63 60.0 83 15 US-10-393-449-52 Sequence 103, 32 63 60.0 83 15 US-10-393-449-52 Sequence 103, 32 63 60.0 83 15 US-10-393-449-52 Sequence 103, 33 63 60.0 83 15 US-10-393-449-52 Sequence 103, 34 63 60.0 83 15 US-10-393-449-52 Sequence 103, 34 63 60.0 83 15 US-10-393-449-52 Sequence 103, 34 63 60.0 83 15 US-10-393-449-52 Sequence 57, 34 63 60.0 84 14 US-10-177-725-99 Sequence 59, 34 63 60.0 84 14 US-10-177-725-51 Sequence 51, 44 63 60.0 91 14 US-10-393-449-51 Sequence 51, 44 63 60.0 91 14 US-10-393-449-51 Sequence 51, 44 63 60.0 91 14 US-10-393-449-51 Sequence 51, 44 63 60.0 91 15 US-10-393-449-51 Sequence 51, 54 63 60.0 91 14 US-10-393-449-51 Seque
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US-10-393-449-89 US-10-393-449-89 US-10-393-449-89 US-10-393-449-90 US-10-177-725-41 US-10-177-725-91 US-10-177-725-91 US-10-393-449-41 US-10-393-449-10 US-10-393-449-10 US-10-393-449-105 US-10-393-449-105 US-10-393-449-105 US-10-393-449-104 US-10-393-449-105 US-10-393-449-104 US-10-393-449-105 US-10-393-449-103 US-10-177-725-103 US-10-393-449-103 US-10-177-725-101 US-10-393-449-103 US-10-177-725-101 US-10-393-449-103 US-10-177-725-101 US-10-393-449-103 US-10-177-725-101 US-10-393-449-101 US-10-393-449-101 US-10-177-725-101
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## ALIGNMENTS

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Query Match Best Local Similarity Batches 17; Conser 1 AXAEAAEKA	APPLICANT: B APPLICANT: B APPLICANT: P ITILB OF INVE FILE REFERENC CURRENT APPLI CURRENT FILING PRIOR APPLICA PRIOR FILING NUMBER OF SEQ SOFTWARE: PAT SEQ ID NO 42 INTYPE: PRT ORGANISM: AF FEATURE: OTHER INFORM OTHER INFORM	RESULT 1  US-10-177-725-42  ; Sequence 42, Applica ; Publication No. US20 ; GENERAL INFORMATION: ; APPLICANT: Anderson
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ch 63. 1 Similarity 68. 17; Conservative 1 AXAEAAEKAAKYAAE 1  -   -   -   -   -   -   -   -   -   -	APPLICANT: Bogenberger, Jako APPLICANT: Peele, Beau R. TITLE OF INVENTION: STRUCTURA TITLE OF INVENTION: STRUCTURA TITLE OF INVENTION: STRUCTURA TITLE OF INVENTION: STRUCTURA TITLE OF INVENTION NUMBER: US CURRENT FILING DATE: 2002-06 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-10-08 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-10-08 RIOR FILING DATE: 1998-10-08 ROMERANE OF SEQ ID NOS: 173 SOFTWARE: Patentin version 3. EQ ID NO 42 LENGTH: 104 TYPE: PRT ORGANISM: Artificial sequenc TEATURE: OTHER INFORMATION: Synthetic 10-1177-725-42	ULT 1 10-177-725-42 requence 42, Application US ublication No. US200301435 ENERAL INFORMATION: APPLICANT: Anderson, David
ch 1 Similarity 63.8%; Score 67 1 Similarity 68.0%; Pred. No 17; Conservative 2; Misma 17; Conservative AARAARAARAARAARAA 25 1 AXABAABKAAKAARAARAA 34 10 AAAAAABAAAKAAABAA 34	APPLICANT: Bogenberger, Jakob M. APPLICANT: Peele, Beau R. TITLE OF INVENTION: STRUCTURALLY BIASED R FILE REFERENCE: A-66900-4/RMS/AMS CURRENT APPLICATION NUMBER: US/10/177,725 CURRENT FILING DATE: 2002-06-20 PRIOR APPLICATION NUMBER: US 09/415,765 PRIOR FILING DATE: 1999-10-08 PRIOR APPLICATION NUMBER: US 09/169,015 PRIOR FILING DATE: 1998-10-08 NUMBER OF SEQ ID NOS: 173 SOFTWARE: Patentin version 3.1 EQ ID NO 42 LENGTH: 104 TYPE: PRT ORGANISM: Artificial sequence TEATURE: OTHER INFORMATION: Synthetic 10-177-725-42	SULT 1 1-10-177-725-42 Sequence 42, Application US/10177725 Publication No. US20030143562A1 GENERAL INFORMATION: APPLICANT: Anderson, David
Scol Prec 2; N CAAKAN	JLY BJ /AMS 5/10/J -20 09/169 09/169	77725
Score 67; DB Pred. No. 0.3 2; Mismatches 7AAKAXA 25           7AAAEAA 34	(ASED 177,73 5,765	U,
Score 67; DB Pred. No. 0.3; ; Mismatches AKAXA 25   :  AAEAA 34	APPLICANT: Begenberger, Jakob M. APPLICANT: Peele, Beau R. TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS CURRENT APPLICATION NUMBER: US/10/17,725 CURRENT FILING DATE: 2002-06-20 PRIOR APPLICATION NUMBER: US 09/415,765 PRIOR FILING DATE: 1999-10-08 PRIOR APPLICATION NUMBER: US 09/169,015 PRIOR FILING DATE: 1998-10-08 PRIOR FILING DATE: 1998-10-08 INVMBER OF SEQ ID NOS: 173 SOFTWARE: Patentin version 3.1 EQ ID NO 42 TYPE: PRT ORGANISM: Artificial sequence FEATURE: OTHER INFORMATION: Synthetic 10-177-725-42	
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Publication No. US20030143562A1
GENERAL INFORMATION:
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Publication No. US20030224412A1
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                                                                                                                                 NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version
SEQ ID NO 42
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                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
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CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, David APPLICANT: Bogenberger, Ja APPLICANT: Peele, Beau R.
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NUMBER OF SEQ ID NOS: 173
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                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                                        LENGTH: 10
TYPE: PRT
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OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
                                           ORGANISM: Artificial sequence FEATURE:
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                   OTHER INFORMATION: synthetic
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Peele, Beau R.
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CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local
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                                                                                                                                       APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson, David
APPLICANT: Bogenberger, J.
APPLICANT: Peele, Beau R.
                                                                                    APPLICANT:
APPLICANT:
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
                                                    APPLICANT:
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APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (37). (68)
OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51,
OTHER INFORMATION: 2, 64-65, and 67-69 can be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE LOCATION: (37)...(68)
OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: synthetic
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                                                                                                                     Cao,
                                                                                                                                   zhou,
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                                                  Barbazuk, Brad
Li, Ping
                                                                                    Boukharov, Andrey
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68.0%;
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Pred. No.
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RESULT 6
US-10-282-122A-55748
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
                                                                         US-10-282-122A-55748
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LENGTH: 827
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                                    Query Match
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NUMBER OF SEQ ID NOS: 204966
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CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                Remaining Prior Application day NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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ORGANISM: Oryza sativa
                                                                                           ORGANISM: Enterobacter cloacae
                                                                                                            LENGTH: 428
TYPE: PRT
                                                                                                                                                                                                                                                                                            DR APPLICATION NUMBER: 60/242,578

DR FILLING DATE: 2000-10-23

DR APPLICATION NUMBER: 60/253,625

DR FILLING DATE: 2000-11-27

DR APPLICATION NUMBER: 60/257,931

DR FILING DATE: 2000-12-22
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                 Match 62.4%;
Local Similarity 62.1%;
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FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                       FILING DATE: 2001-02-16
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 18; Conservative
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Zamudio, car
Zamudio, car
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                                                                                                                                                                                      Application data removed - See File Wrapper or PALM D NOS: 78614
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54.5%;
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                 Score 65.5; Di
Pred. No. 2.2;
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Pred. No. 4;
 Mismatches
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NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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                                                                                                                                           ; OTHER INFORMATION: Synthetic peptide US-10-667-004-24
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                                                           Query Match
Best Local S
Matches 15
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APPLICANT: INTEL CORPORATION
APPLICANT: CHAN, Selena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/10667004 Publication No. US20040126820A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1 SEQ ID NO 24
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Best Local Similarity
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APPLICANT: YAMAXAWA, Mineo
APPLICANT: YAMAXAWA, Mineo
TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATION TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
FILE REFERENCE: INTEL1310-1(P14240X)
CURRENT APPLICATION NUMBER: US/10/667,004
CURRENT FILING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: US 10/251,152
PRIOR FILING DATE: 2002-09-20
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 10/251,152
PRIOR FILING DATE: 2002-09-20
NUMBER OF OTHER PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR DATE: 2002-09-20
                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 26
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FILE REFERENCE: INTELL310-1 (P14240X)
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APPLICANT: CHAN, Selena
APPLICANT: SU, Xing
APPLICANT: YAMAKAWA, Mineo
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/667,004
                                                                                                                                                                                 ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                         TYPE: PRT
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2 XAEAAEKAAKYAAEAAEKAAKAX 24 : | | | | | : | : | | | | | | | : | :
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                                                             61.0%;
larity 65.2%;
Conservative
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65.2%;
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                                                                                Score 64; I
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Pred. No. 0.
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                                                                                                       DB 16; Length 28;
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US-10-177-725-40
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Best Local S
Matches 18
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Matches
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Publication No.
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                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
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APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
FILE REFERENCE: A-66900-4/RWS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
CURRENT FILING DATE: 2002-06-20
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APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Anderson, David
APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial sequence
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                                                                                                                                                                                               OTHER INFORMATION: synthetic
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les 18; Conservative
                                                                                                                     Similarity
                                                          AXAEAAEKAAKYAAEAAEKAAKAXA 25
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No. US20030143562A1
                                                                                                  Conservative
                                                                                                                 61.0%;
72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.0%;
                                                                                              ; Score 64; DB; Pred. No. 0.73
2; Mismatches
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Pred. No.
                        31
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                                                                                                                   DB 14;
0.73;
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                                                                                                                                     Length 104;
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Query Match
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CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin version 3.1
SEQ ID NO 90
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US-10-177-725-90
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 89
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CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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APPLICANT: Bogenberger, J
APPLICANT: Peele, Beau R.
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APPLICANT: Bogenberger, J
APPLICANT: Peele, Beau R.
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
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APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
    FEATURE:
OTHER INFORMATION: synthetic
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (37)...(68)
OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50,
OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
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Peele, Beau R.
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Pred. No. 0.73;
2; Mismatches
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3 can be
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59-6

Best Local Similarity

61.0%; 72.0%;

Score 64; DB 14; Pred. No. 0.73;

Length 104;

59-6

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US-10-393-449-40
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Publication No.
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   Query Match
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Publication No.
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
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CURRENT FILING DATE: 2003-03-18
                                                                                                                                                                       SOFTWARE:
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PRIOR FILING DATE: 1998-10-08
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                                                        OTHER INFORMATION:
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                                                                             FEATURE:
                                                                                           ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: Bogenberger, Jakob M.
PPLICANT: Peele, Beau R.
ITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED
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TLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                                                                                  ENGTH: 104
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FILING DATE: 1999-10-08
APPLICATION NUMBER: US 09/169,015
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US-10-393-449-90
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US-10-393-449-89
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SEQ ID NO 90
LENGTH: 104
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                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF THE STATE OF THE
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
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SOFTWARE: PatentIn version 3.1
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CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
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PRIOR FILING DATE: 1999-10-08
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APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SFILE REFERENCE: RIGL-007CIP3
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OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 'OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
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Peele, Beau R.
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Peele, Beau R.
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72.0%;
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Publication No.
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APPLICANT: Peele, Beau R.
TITLE OF THE TITLE OF TH
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APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
SOFTWARE: P
                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                      APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED
FILE REFERENCE: A-66900-4/RMS/AMS
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, David
APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
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PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
                                                               NUMBER OF SEQ ID NOS:
                                                                                       PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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US-10-393-449-91
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CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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                                                                                                                                                                                                               Sequence 91, Application US/10393449 Publication No. US20030224412A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Publication No.
FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
                                                                                                                     APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Beele, Beau R.
TITLE OF THE STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SCRIPTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SCRIPTION REFERENCE: RIGL-007CIP3
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NAME/KEY: MISC FEATURE
LOCATION: (37). (68)
OTHER INFORMATION: "Xaa" at
OTHER INFORMATION: 1, 63-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: synthetic
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ORGANISM: Artificial sequence
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18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                   AAAAAEAAAK-AAAAAEAAAKAAA
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Pred. No. 0.85
2; Mismatches
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Pred. No. 0.85
2; Mismatches
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any amino
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US-10-177-725-105
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CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 11988-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin version 3.1
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                                                                                                Sequence 105, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 55
LENGTH: 59
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
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Best Local :
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Publication No. US20030143562A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                     APPLICANT: Anderson, David APPLICANT: Bogenberger, Ja APPLICANT: Peele, Beau R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: "Xaa" at positions 37-39, 41-43, 45-46, 48-50, 52-53, 55-57, 59. OTHER INFORMATION: 1, 63-64 and 66-68 can be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE LOCATION: (37)..(68)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
ITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
ILE REFERENCE: A-66900-4/RMS/AMS
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                                                            Jakob M.
                                                                                                                                                                                                                                                                                                                                        pred. No. 0.53
Mismatches
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0.53;
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RESULT 24 US-10-393-449-105

GENERAL INFORMATION: APPLICANT: Anderson, Sequence 105, Appropriation No.

Application US/10393449 o. US20030224412A1

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CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR PILICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC PEATURE

LOCATION: (30)...(46)

OTHER INFORMATION: "Xaa" at positions 30-32, 34-36, 38-39, 41-43, and THER INFORMATION: ny amino acid

US-10-177-725-105
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US-10-393-449-55
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                                                                              Matches
                                                                                                                 Query Match
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Best Local
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TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SOFILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR PILING DATE: 2002-06-20
PRIOR PILING DATE: 2002-06-20
PRIOR PILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anderson, David APPLICANT: Bogenberger, Japplicant: Peele, Beau R.
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/169,015 PRIOR FILING DATE: 1998-10-08
                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial sequence FEATURE:
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Local Similarity 66.7%;
nes 16; Conservative
                                                                            Local Similarity 66.7
les 16; Conservative
                               2 XAEAAEKAAKYAAEAAEKAAKAXA 25
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    DAAAAEAAAKAAAEAAAKAAAEAA 27
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                                                                                                                                                                                                                                                                                                   version 3.1
                                                                                               60.0%;
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Pred. No. 0.53;
                                                                                               Score 63; I
Pred. No. 0.
                                                                            Mismatches
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                                                                                                                   Length 59
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; Sequence 104, Application US/10177725
                 RESULT 26
US-10-177-725-104
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PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 54
LENGTH: 67
                                                                                                                                                                       Matches
                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54, Application US/10177725
Publication No. US20030143562A1
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PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
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                                                                                                                                                                                                                                                                               LENGTH: 67
TYPE: PRT
ORGANISM: Artificial sequence
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LOCATION: (30)..(46)
OTHER INFORMATION: "Xaa" at positions 30-32, 34-36, 38-39, 41-43, and 45-46 can be OTHER INFORMATION: ny amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 59
TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                2 ХАЕААЕКААКУААЕААЕКААКАХА 25
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                                                                                            DAAAAEAAKAAAEAAAKAAAEAA 27
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Pred. No. 0.61
2; Mismatches
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Pred. No. 0.
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0.53;
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; OTHER INFORMATION: synthetic US-10-393-449-54
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PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 104
                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin version 3.1
SEQ ID NO 54
LENGTH: 67
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                                                                                Matches
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CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
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APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
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CURRENT FILLING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
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APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
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TYPE: PRT
ORGANISM: Artificial sequence
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OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be OTHER INFORMATION: ny amino acid
                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
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OTHER INFORMATION: synthetic
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16; Conser
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DAAAAEAAAKAAAEAAAKAAAEAA 27
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Peele, Beau R.
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Pred. No. 0.61
2; Mismatches
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Pred. No. 0.61;
2; Mismatches
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US-10-393-449-104
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Publication No.
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  Best Local Similarity Matches 16; Conserv
                                                Query Match
                                                                                             OTHER INFORMATION: synthetic -10-177-725-53
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PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
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CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
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APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
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APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
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PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
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OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be OTHER INFORMATION: ny amino acid
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                                                                                                                                             FEATURE:
                                                                                                                                                              ORGANISM: Artificial sequence
                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                            ID NO 53
ENGTH: 75
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Similarity 66.7%;
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Peele, Beau R.
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    Conservative
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                          60.0%; Score 63; DB 14; Length 75; 66.7%; Pred. No. 0.69;
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US-10-177-725-103
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 103
                                                                                                        SOFTWARE: PatentIn version 3.1 SEQ ID NO 53
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Best Local Similarity
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PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1996-10-08
NUMBER OF SEQ ID NOS: 173
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CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                       FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
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LOCATION: (38)...(54)
OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can OTHER INFORMATION: ny amino acid
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                       FEATURE:
                                                              TYPE: PRT
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OTHER INFORMATION: synthetic
OTHER INFORMATION: synthetic
                                       ORGANISM: Artificial sequence
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Peele, Beau R.
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Peele, Beau R.
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66.7%;
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Pred. No. 0.
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US-10-177-725-52
; Sequence 52, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
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US-10-393-449-103
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SEQ ID NO 103
LENGTH: 75
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Best Local Similarity
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                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 52
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                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, David APPLICANT: Bogenberger, J. APPLICANT: Peele, Beau R.
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PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-11-08
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APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
                                                                                                      PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                   TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
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CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
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LENGTH: 83
TYPE: PRT
ORGANISM: Artificial sequence
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16; Conserv
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5. US20030224412A1
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Pred. No. 0.69
2; Mismatches
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Pred. No. 0.69;
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2; Mismatches
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RESULT 35
US-10-393-449-52
; Sequence 52, Application US/10393449
; Publication No. US20030224412A1
; Publication No. US20030224412A1
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; OTHER INFORMATION: synthetic
US-10-177-725-52
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CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
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Best Local Similarity
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                                  APPLICANT: Anderson, David
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bedele, Beau R.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT :
FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR PILING DATE: 1998-10-08
PRIOR PILING DATE: 1998-10-08
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APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peelle, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERATURE: NISC_FEATURE NAME/KEY: MISC_FEATURE LOCATION: (38)..(54)
OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, OTHER INFORMATION: ny amino acid
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ORGANISM: Artificial sequence
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                      SEQ ID NOS: 173
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Pred. No. 0.77;
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Pred. No. 0.
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0.77;
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RESULT 37
US-10-177-725-49
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LENGTH: 83
                                                                                                                                               Sequence 49, Application No. US20 GENERAL INFORMATION:
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SEQ ID NO 102
LENGTH: 83
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Best Local Similarity
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PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
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CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
                                                                                       APPLICANT: Anderson, David
APPLICANT: Bogenberger, Ja
APPLICANT: Peele, Beau R.
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             CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
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                                                   TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
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TYPE: PRT
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COCHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, OTHER INFORMATION: ny amino acid
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OTHER INFORMATION: synthetic
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APPLICATION NUMBER: US 09/415,765
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                                                                                                                                                                                                                                                                                                                      1 AXAEAAEKAAKYAAEAAEKAAKAX 24
                                                                                                                                                                                                                                                                                                                                                                              60.0%;
Similarity 66.7%;
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Peele, Beau R.
                                                                                                                                                                 Application US/10177725
o. US20030143562A1
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                                                                                                             Jakob M.
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Pred. No. 0.
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                                                                                                                                        RESULT 39
US-10-393-449-49
US-10-393-449-49
; Sequence 49, Application US/10393449
; Publication No. US20030224412A1
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US-10-177-725-99
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GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Beele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON FILE REFERENCE: RIGL-007CIP3
CURRENT APPLICATION NUMBER: US/10/393,449
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 99
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
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Best Local Similarity
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CURRENT FILING DATE: 2002-06-20
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APPLICANT: Bogenberger, Ja
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: A-66900-4/RMS/AMS
                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (29). (60)
OTHER INFORMATION: "Xaa" at positions 29-31, 33-35, 37-38, 40-42,
OTHER INFORMATION: 3, 55-56, and 58-60 can be any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: synthetic FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial sequence
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Peele, Beau R.
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Pred. No. 0.
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Pred. No. 0.82;
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RESULT 41
US-10-177-725-51
; Sequence 51, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
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US-10-393-449-99
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 99
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Publication No. US20030224412A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
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PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
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APPLICANT: Bogenberger, Jakob M.
APPLICANT: Beele, Beau R.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
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PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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PRIOR FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE LOCATION: (29). (60)
OTHER INFORMATION: "Xaa" at positions 29-31, 33-35, 37-38, 40-42, OTHER INFORMATION: 3, 55-56, and 58-60 can be any amino acid
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TYPE: PRT
ORGANISM: Artificial sequence
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TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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Similarity 66.7%;
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Pred. No. 0.82;
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Pred. No. 0.82;
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US-10-393-449-51
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Sequence 51, Application US/10393449 Publication No. US20030224412A1
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APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Beele, Beau R.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEI
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
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US-10-177-725-101
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SEQ ID NO 101
LENGTH: 91
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 51
                                                                          Matches
                                                                                                            Query Match
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APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
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CURRENT FILING DATE: 2002-06-20
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PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
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ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                    NAME/KEY: MISC_PEATURE LOCATION: (38)..(54)
COCATION: (38)..(54)
OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be OTHER INFORMATION: ny amino acid
                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: synthetic
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                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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nes 16; Conserv
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                                  1 AXAEAAEKAAKYAAEAAEKAAKAX 24
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AAKAAAEAAAKAAAEAAAKAAAAK 88
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o. US20030143562A1
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                                                                          Conservative
                                                                                          66.7%;
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                                                                        Score 63; DB
Pred. No. 0.85
2; Mismatches
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Pred. No. 0.85;
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                                                                                          0.85;
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                                                                                                            Length 91;
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US-10-393-449-101
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                                                          Query Match
Best Local Similarity 66.7
16; Conservative
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BOGENberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT
FILE REFERENCE: RIGL-007CIP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: US 10/177,725
PRIOR FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/393,449
CURRENT FILING DATE: 2003-03-18
                                                                                                                                FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (38)..(54)
OTHER INFORMATION: "Xaa" at positions 38-40, 42-44, 46-47, 49-51, and 53-54 can be
OTHER INFORMATION: ny amino acid
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1 EQ ID NO 101
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/169,015
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                                                                                                                                                                                                                                                                                            LENGTH: 91
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q ID NO 51
LENGTH: 91
TYPE: PRT
ORGANISM: Artificial seguence
                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLICANT: Anderson, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2002-06-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 АХАЕААЕКААКҮААЕААЕКААКАХ 24
  AAKAAAEAAAKAAAEAAAKAAAAK 88
                                    AXAEAAEKAAKYAAEAAEKAAKAX 24
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5. US20030224412A1
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                                                                        60.0%; Score 63; DB 66.7%; Pred. No. 0.89 tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.0%; Score 63; DB 1:
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                                                                                                              Length 91
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                                                                                                                                                                                                                                                                         SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47, Application US/10177725
Publication No. US20030143562A1
                                                                          Matches
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/415,765 PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                TILE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SCILE REFERENCE: A-66900-4/RMS/AMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson, David
                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                       ENGTH: 104
                                                                        Local Similarity 66.7
nes 16; Conservative
79
                                    1 AXAEAAEKAAKYAAEAAEKAAKAX 24
AAKAAAEAAKAAAEAAAKAAAAK 102
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Peele, Beau R.
                                                                                            60.0%;
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Pred. No. 0.98
2; Mismatches
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Search completed: July 11, 2005, 10:00:02 Job time: 160 secs

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